SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
      Hilbun, Erin
      Donoho, Gregory
      Scoville, John
      Wattler, Frank
      Friedrich, Glenn
      Abuin, Alejandro
      Zambrowicz, Brian
      Sands, Arthur T.

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Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
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6

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Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
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Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
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Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
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His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
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Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
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Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
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            195                 200                 205

Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220

Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240

His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255

Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                260                 265                 270

Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                 280                 285

Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300

Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305                 310                 315                 320
```

7

```
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
              325                 330                 335
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
              340                 345                 350
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
              355                 360                 365
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
        370                 375                 380
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
385                 390                 395                 400
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                  405                 410                 415
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                  420                 425                 430
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
          435                 440                 445
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
      450                 455                 460
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
465                 470                 475                 480
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                  485                 490                 495
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
              500                 505                 510
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
          515                 520                 525
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
      530                 535                 540
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
545                 550                 555                 560
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                  565                 570                 575
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
              580                 585                 590
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
          595                 600                 605
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
      610                 615                 620
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
625                 630                 635                 640
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                  645                 650                 655
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
              660                 665                 670
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
          675                 680                 685
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
      690                 695                 700
Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
705                 710                 715                 720
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
                  725                 730                 735
Tyr Gly Asp Arg Arg Phe Trp Asn Ala Val Ser Phe Tyr Thr Glu Ala
              740                 745                 750
Ser Tyr Leu His Phe Pro Thr Phe His Ala Glu Phe Ser Ala Asp Ile
          755                 760                 765
```

8

```
Ser Phe Phe Phe Lys Thr Thr Ala Leu Ser Gly Val Phe Leu Glu Asn
    770                 775             780
Leu Gly Ile Lys Asp Phe Ile Arg Leu Glu Ile Ser Ser Pro Ser Glu
785             790             795                 800
Ile Thr Phe Ala Ile Asp Val Gly Asn Gly Pro Val Glu Leu Val Val
            805             810             815
Gln Ser Pro Ser Leu Leu Asn Asp Asn Gln Trp His Tyr Val Arg Ala
            820             825             830
Glu Arg Asn Leu Lys Glu Thr Ser Leu Gln Val Asp Asn Leu Pro Arg
        835             840             845
Ser Thr Arg Glu Thr Ser Glu Glu Gly His Phe Arg Leu Gln Leu Asn
    850             855             860
Ser Gln Leu Phe Val Gly Gly Thr Ser Ser Arg Gln Lys Gly Phe Leu
865             870             875                 880
Gly Cys Ile Arg Ser Leu His Leu Asn Gly Gln Lys Met Asp Leu Glu
            885             890             895
Glu Arg Ala Lys Val Thr Ser Gly Val Arg Pro Gly Cys Pro Gly His
            900             905             910
Cys Ser Ser Tyr Gly Ser Ile Cys His Asn Gly Gly Lys Cys Val Glu
        915             920             925
Lys His Asn Gly Tyr Leu Cys Asp Cys Thr Asn Ser Pro Tyr Glu Gly
    930             935             940
Pro Phe Cys Lys Lys Glu Val Ser Ala Val Phe Glu Ala Gly Thr Ser
945             950             955                 960
Val Thr Tyr Met Phe Gln Glu Pro Tyr Pro Val Thr Lys Asn Ile Ser
            965             970             975
Leu Ser Ser Ser Ala Ile Tyr Thr Asp Ser Ala Pro Ser Lys Glu Asn
            980             985             990
Ile Ala Leu Ser Phe Val Thr Thr Gln Ala Pro Ser Leu Leu Leu Phe
        995             1000            1005
Ile Asn Ser Ser Ser Gln Asp Phe Val Val Val Leu Leu Cys Lys Asn
    1010            1015            1020
Gly Ser Leu Gln Val Arg Tyr His Leu Asn Lys Glu Glu Thr His Val
1025            1030            1035                1040
Phe Thr Ile Asp Ala Asp Asn Phe Ala Asn Arg Arg Met His His Leu
            1045            1050            1055
Lys Ile Asn Arg Glu Gly Arg Glu Leu Thr Ile Gln Met Asp Gln Gln
        1060            1065            1070
Leu Arg Leu Ser Tyr Asn Phe Ser Pro Glu Val Glu Phe Arg Val Ile
        1075            1080            1085
Arg Ser Leu Thr Leu Gly Lys Val Thr Glu Asn Leu Gly Leu Asp Ser
    1090            1095            1100
Glu Val Ala Lys Ala Asn Ala Met Gly Phe Ala Gly Cys Met Ser Ser
1105            1110            1115                1120
Val Gln Tyr Asn His Ile Ala Pro Leu Lys Ala Ala Leu Arg His Ala
            1125            1130            1135
Thr Val Ala Pro Val Thr Val His Gly Thr Leu Thr Glu Ser Ser Cys
            1140            1145            1150
Gly Phe Met Val Asp Ser Asp Val Asn Ala Val Thr Thr Val His Ser
        1155            1160            1165
Ser Ser Asp Pro Phe Gly Lys Thr Asp Glu Arg Glu Pro Leu Thr Asn
    1170            1175            1180
Ala Val Arg Ser Asp Ser Ala Val Ile Gly Gly Val Ile Ala Val Val
1185            1190            1195                1200
Ile Phe Ile Ile Phe Cys Ile Ile Gly Ile Met Thr Arg Phe Leu Tyr
            1205            1210            1215
```

9

```
Gln His Lys Gln Ser His Arg Thr Ser Gln Met Lys Glu Lys Glu Tyr
            1220                 1225                1230
Pro Glu Asn Leu Asp Ser Ser Phe Arg Asn Glu Ile Asp Leu Gln Asn
        1235                 1240                1245
Thr Val Ser Glu Cys Lys Arg Glu Tyr Phe Ile
    1250                 1255


<210> 5
<211> 108
<212> DNA
<213> homo sapiens


<400> 5
atggattctt taccacggct gaccagcgtt ttgactttgc tgttctctgg cttgtggcat        60
ttaggattaa cagcgacaaa ctacctttgc aggaaacatg aatgctga                    108


<210> 6
<211> 35
<212> PRT
<213> homo sapiens


<400> 6
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1               5                  10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Leu Cys Arg Lys
            20                  25                  30
His Glu Cys
        35


<210> 7
<211> 753
<212> DNA
<213> homo sapiens


<400> 7
atggattctt taccacggct gaccagcgtt ttgactttgc tgttctctgg cttgtggcat        60
ttaggattaa cagcgacaaa ctacaactgt gatgatccac tagcatccct gctctctcca       120
atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg       180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg       240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct       300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac       360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac       420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat       480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt       540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact       600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag agatgggggt cctgttccat       660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta       720
cacctcaatt tggtggtttg tagttctcct tga                                    753


<210> 8
<211> 250
<212> PRT
<213> homo sapiens


<400> 8
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser

                                    10
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        1                   5                       10                      15
      Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
                      20                  25                      30
      Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
              35                  40                      45
      Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
          50                  55                      60
      Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
      65                  70                  75                      80
      Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                      85                  90                      95
      Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
                  100                 105                 110
      Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
              115                 120                 125
      Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
          130                 135                 140
      His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
      145                 150                 155                 160
      Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                      165                 170                 175
      Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                  180                 185                 190
      Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
              195                 200                 205
      Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
          210                 215                 220
      Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
      225                 230                 235                 240
      His Leu Asn Leu Val Val Cys Ser Ser Pro
                      245                 250

<210> 9
<211> 840
<212> DNA
<213> homo sapiens

<400> 9
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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct     300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac     360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac     420
cacaagctat gcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt     540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact     600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat     660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta     720
cacctcaatt tgggtgacag caaagcgcgg ctaagcactt gccctctgcc accctgggca     780
gcctcctgga tgaccagcac tggcactygg tcctcattga gcgggtgggc aagcaggtga     840

<210> 10
<211> 279
<212> PRT
```

11

<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(279)
<223> Xaa = Any Amino Acid

<400> 10
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
1   5   10   15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
                20   25   30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35   40   45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
        50   55   60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65   70   75   80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85   90   95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100   105   110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115   120   125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130   135   140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145   150   155   160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165   170   175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                180   185   190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195   200   205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210   215   220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225   230   235   240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Thr Cys Pro Leu
                245   250   255
Pro Pro Trp Ala Ala Ser Trp Met Thr Ser Thr Gly Thr Xaa Ser Ser
                260   265   270
Leu Ser Gly Trp Ala Ser Arg
        275

<210> 11
<211> 1749
<212> DNA
<213> homo sapiens

<400> 11
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ttaggattaa cagcgacaaa ctacaactgt gatgatccac tagcatccct gctctctcca   120
atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg   180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg   240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct   300

12

```
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac    360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac    420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgccct  ggaatggaat    480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt    540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact    600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat    660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta    720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg    780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag    840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc    900
ttagacattg actatgagct tagttttgga ggaattccag taccaggaaa acctgggacc    960
tttttaaaga aaaacttcca tggatgcatc gaaaaccttt actacaatgg agtaaacata   1020
attracctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cactttttcc   1080
tgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg   1140
ctgcccggca cccccaaat  tgatgggctc tcagtgagtt ccagtttcg  aacatggaac   1200
aaggatggtc tgcttctgtc cacagagctg tctgagggct cgggaaccct gctgctgagc   1260
ctggagggtg gaatcctgag actcgtgatt cagaaaatga cagaacgcgt agctgaaatc   1320
ctcacaggca gcaacttgaa tgatggcctg tggcactcgg ttagcatcaa cgccaggagg   1380
aaccgcatca cgctcactct ggatgatgaa gcagcacccc cggctccaga cagcacttgg   1440
gtgcagattt attctggaaa tagctactat tttggaggtg tttgccaaac tactgtgaac   1500
atggaggaag ctgctcccag tcctggacta ccttctattg taactgcagt gacacaagtt   1560
acactggtgc cacctgccac aactccatct acgagcaatc ctgcgaggtg tacaggcacc   1620
agggaatac  agccggcttc ttctacatcg actcagatgg cagcggccca ctgggacctc   1680
tccaggtgta ctgcaatatc actgaggaca agatctggac atcagtgcag cacaacaata   1740
cagagctga                                                           1749
```

<210> 12
<211> 582
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(582)
<223> Xaa = Any Amino Acid

<400> 12
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Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1               5                  10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
                20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
        50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
               100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
           115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
       130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
```

13

```
        145                     150                     155                     160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                    165                     170                     175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                180                     185                     190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                     200                     205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
        210                     215                     220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
    225                     230                     235                     240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                    245                     250                     255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                260                     265                     270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                     280                     285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
        290                     295                     300
Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
    305                     310                     315                     320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
                    325                     330                     335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
                340                     345                     350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
            355                     360                     365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
        370                     375                     380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
    385                     390                     395                     400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                405                     410                     415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
                420                     425                     430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
            435                     440                     445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
        450                     455                     460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
    465                     470                     475                     480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Val Cys Gln
                485                     490                     495
Thr Thr Val Asn Met Glu Glu Ala Ala Pro Ser Pro Gly Leu Pro Ser
                500                     505                     510
Ile Val Thr Ala Val Thr Gln Val Thr Leu Val Pro Pro Ala Thr Thr
            515                     520                     525
Pro Ser Thr Ser Asn Pro Ala Arg Cys Thr Gly Thr Arg Gly Ile Gln
        530                     535                     540
Pro Ala Ser Ser Thr Ser Thr Gln Met Ala Ala Ala His Trp Asp Leu
    545                     550                     555                     560
Ser Arg Cys Thr Ala Ile Ser Leu Arg Thr Arg Ser Gly His Gln Cys
                565                     570                     575
Ser Thr Thr Ile Gln Ser
                580
```

14

<210> 13
<211> 1605
<212> DNA
<213> homo sapiens

<400> 13
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atggattctt taccacggct gaccagcgtt ttgactttgc tgttctctgg cttgtggcat      60
ttaggattaa cagcgacaaa ctacaactgt gatgatccac tagcatccct gctctctcca     120
atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct     300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac     360
aaacaagaag acagcatctg gaccttgca ggaaacatga atgctgacag cgtggtgcac      420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt     540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact     600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat     660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta     720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg     780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag     840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc     900
ttagacattg actatgaggg caatgtcact ttttcctgct ccgaaccaca gattgtgccc     960
atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat    1020
gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca    1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc    1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat    1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat    1260
gatgaagcag cacccccggc tccagacagc acttgggtgc agatttattc tggaaatagc    1320
tactattttg gaggtgtttg ccaaactact gtgaacatgg aggaagctgc tcccagtcct    1380
ggactacctt ctattgtaac tgcagtgaca caagttacac tggtgccacc tgccacaact    1440
ccatctacga gcaatcctgc gaggtgtaca ggcaccaggg aatacagcc ggcttcttct      1500
acatcgactc agatggcagc ggcccactgg gacctctcca ggtgtactgc aatatcactg    1560
aggacaagat ctggacatca gtgcagcaca acaatacaga gctga                     1605
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<210> 14
<211> 534
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(534)
<223> Xaa = Any Amino Acid

<400> 14
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Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
1               5                   10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
```

```
                     85                      90                      95
      Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
                  100                     105                     110
      Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
              115                     120                     125
      Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
          130                     135                     140
      His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
      145                     150                     155                     160
      Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                      165                     170                     175
      Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                  180                     185                     190
      Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
              195                     200                     205
      Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
          210                     215                     220
      Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
      225                     230                     235                     240
      His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                      245                     250                     255
      Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                  260                     265                     270
      Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
                  275                     280                     285
      Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
          290                     295                     300
      Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
      305                     310                     315                     320
      Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
                      325                     330                     335
      Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
                  340                     345                     350
      Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                  355                     360                     365
      Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
          370                     375                     380
      Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
      385                     390                     395                     400
      Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                      405                     410                     415
      Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                  420                     425                     430
      Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Val Cys Gln
              435                     440                     445
      Thr Thr Val Asn Met Glu Glu Ala Ala Pro Ser Pro Gly Leu Pro Ser
          450                     455                     460
      Ile Val Thr Ala Val Thr Gln Val Thr Leu Val Pro Pro Ala Thr Thr
      465                     470                     475                     480
      Pro Ser Thr Ser Asn Pro Ala Arg Cys Thr Gly Thr Arg Gly Ile Gln
                  485                     490                     495
      Pro Ala Ser Ser Thr Ser Thr Gln Met Ala Ala Ala His Trp Asp Leu
                  500                     505                     510
      Ser Arg Cys Thr Ala Ile Ser Leu Arg Thr Arg Ser Gly His Gln Cys
              515                     520                     525
      Ser Thr Thr Ile Gln Ser
```

16

<210> 15
<211> 2238
<212> DNA
<213> homo sapiens

<400> 15

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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg    180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg    240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct    300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac    360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac    420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat    480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt    540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact    600
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cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg    780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag    840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc    900
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attracctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cacttttttcc   1080
tgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg   1140
ctgcccggca cccccaaat tgatgggctc tcagtgagtt tccagtttcg aacatggaac   1200
aaggatggtc tgcttctgtc cacagagctg tctgagggct cgggaaccct gctgctgagc   1260
ctggagggtg gaatcctgag actcgtgatt cagaaaatga cagaacgcgt agctgaaatc   1320
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aaccgcatca cgctcactct ggatgatgaa gcagcacccc cggctccaga cagcacttgg   1440
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cacattgatc tgtgtagcat caaagacagg tgtttgccaa actactgtga acatggagga   1680
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tactgcaata tcactgagga caagatctgg acatcagtgc agcacaacaa tacagagctg   1920
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attggcggt ccaatgaaag gcacccttac tggggaggtt cccctcctgg ggtccagcag   2160
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gacaaggatg aatggtaa                                               2238
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<210> 16
<211> 745
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(745)
<223> Xaa = Any Amino Acid

<400> 16

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
            165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
    195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
            245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
    275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
305                 310                 315                 320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
            325                 330                 335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
            340                 345                 350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
    355                 360                 365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
    370                 375                 380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385                 390                 395                 400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
            405                 410                 415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
            420                 425                 430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
```

18

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                435                      440                      445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
    450                      455                      460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465                      470                      475                      480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                485                      490                      495
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
                500                      505                      510
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
            515                      520                      525
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
    530                      535                      540
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
545                      550                      555                      560
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                565                      570                      575
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
            580                      585                      590
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
    595                      600                      605
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
    610                      615                      620
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
625                      630                      635                      640
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
                645                      650                      655
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
            660                      665                      670
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
            675                      680                      685
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
    690                      695                      700
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
705                      710                      715                      720
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                725                      730                      735
Asn Cys Asp Ala Asp Lys Asp Glu Trp
            740                      745
```

<210> 17
<211> 2094
<212> DNA
<213> homo sapiens

<400> 17
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atggctttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg      180
agagttggaa ctggcggttg tccccagca gattccaatg ctcaacagtg gctccagatg      240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct      300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac      360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac      420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat      480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt      540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact      600
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19
```

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ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat    660
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cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg    780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag    840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc    900
ttagacattg actatgaggg caatgtcact ttttcctgct ccgaaccaca gattgtgccc    960
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gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca   1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc   1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat   1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat   1260
gatgaagcag caccccccggc tccagacagc acttgggtgc agatttattc tggaaatagc   1320
tactattttg gagggtgccc cgacaatctc accgattccc aatgtttaaa tcccattaag   1380
gctttccaag gctgcatgag gctcatcttt attgataacc agcccaagga cctcatttca   1440
gttcagcaag gttccctggg gaattttagt gatttacaca ttgatctgtg tagcatcaaa   1500
gacaggtgtt tgccaaacta ctgtgaacat ggaggaagct gctcccagtc ctggactacc   1560
ttctattgta actgcagtga cacaagttac actggtgcca cctgccacaa ctccatctac   1620
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tcagatggca gcggcccact gggacctctc caggtgtact gcaatatcac tgaggacaag   1740
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gagaagccct atgccatggc cttggactac gggggcagca tggaacagct ggaggccgtg   1860
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ctcaacacgc cggatggaac accatttacc tggtggattg ggcggtccaa tgaaaggcac   1980
ccttactggg gaggttcccc tcctggggtc cagcagtgtg agtgtggcct agacgagagc   2040
tgcctggaca ttcagcactt ttgcaattgc gacgctgaca aggatgaatg gtaa          2094
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<210> 18
<211> 697
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(697)
<223> Xaa = Any Amino Acid

<400> 18

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
```
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20
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      145                     150                     155                     160
      Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                          165                     170                     175
      Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                          180                     185                     190
      Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
                  195                     200                     205
      Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
          210                     215                     220
      Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
      225                     230                     235                     240
      His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                          245                     250                     255
      Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                  260                     265                     270
      Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
                  275                     280                     285
      Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
          290                     295                     300
      Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
      305                     310                     315                     320
      Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
                          325                     330                     335
      Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
                  340                     345                     350
      Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                  355                     360                     365
      Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
          370                     375                     380
      Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
      385                     390                     395                     400
      Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                          405                     410                     415
      Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                  420                     425                     430
      Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                  435                     440                     445
      Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
          450                     455                     460
      Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
      465                     470                     475                     480
      Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                          485                     490                     495
      Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
                  500                     505                     510
      Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                  515                     520                     525
      Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
          530                     535                     540
      Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
      545                     550                     555                     560
      Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                          565                     570                     575
      Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
                  580                     585                     590
      Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
```

21

```
              595                      600                      605
   Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
       610                      615                      620
   Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
   625                      630                      635                      640
   Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                       645                      650                      655
   Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
                   660                      665                      670
   Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
               675                      680                      685
   Asn Cys Asp Ala Asp Lys Asp Glu Trp                          .
       690                      695
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<210> 19
<211> 2520
<212> DNA
<213> homo sapiens

<400> 19

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atggctttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
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gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac     360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac     420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt     540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact     600
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attracctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cactttttcc    1080
tgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg    1140
ctgcccggca cccccaaat tgatgggctc tcagtgagtt ccagtttcg aacatggaac    1200
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tactgcaata tcactgagga caagatctgg acatcagtgc agcacaacaa tacagagctg    1920
acccgagtgc ggggcgctaa ccctgagaag ccctatgcca tggccttgga ctacgggggc    1980
agcatggaac agctggaggc cgtgatcgac ggctctgagc actgtgagca ggaggtggcc    2040
taccactgca ggaggtcccg cctgctcaac acgccggatg gaacaccatt tacctggtgg    2100
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22

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tgtgagtgtg gcctagacga gagctgcctg gacattcagc acttttgcaa ttgcgacgct    2220
gacaaggatg aatggacaaa tgatactggc tttctttcct tcaaagacca cttgcctgtc    2280
actcagatag ttatcactga taccgacaga tcaaactcag aagccgcttg gagaattggt    2340
cccttgcgtt gctatggtga ccgtgagtac aaaatcgaaa gaagctttct ctctgcatta    2400
catgagcaca agatgttctt actcccttat ccctttttccc tgcagtgtgc cctagtcttg    2460
aaaattatcc acatgtccag tgctttccca taccccactg aaaacgataa accatgttga    2520
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<210> 20
<211> 839
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(839)
<223> Xaa = Any Amino Acid

<400> 20

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
        195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
        275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
```

23

Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
305   310   315   320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
                325   330   335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
                340   345   350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
            355   360   365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
        370   375   380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385   390   395   400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                405   410   415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
            420   425   430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
        435   440   445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
    450   455   460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465   470   475   480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                485   490   495
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
            500   505   510
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
        515   520   525
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
    530   535   540
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
545   550   555   560
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                565   570   575
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
            580   585   590
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
            595   600   605
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
        610   615   620
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
625   630   635   640
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
                645   650   655
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
            660   665   670
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
        675   680   685
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
    690   695   700
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
705   710   715   720
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                725   730   735
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
            740   745   750

24

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Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
        755                 760                 765
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
    770                 775                 780
Tyr Gly Asp Arg Glu Tyr Lys Ile Glu Arg Ser Phe Leu Ser Ala Leu
785                 790                 795                 800
His Glu His Lys Met Phe Leu Leu Pro Tyr Pro Phe Ser Leu Gln Cys
                805                 810                 815
Ala Leu Val Leu Lys Ile Ile His Met Ser Ser Ala Phe Pro Tyr Pro
                820                 825                 830
Thr Glu Asn Asp Lys Pro Cys
        835


<210> 21
<211> 2376
<212> DNA
<213> homo sapiens


<400> 21
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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg    180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg    240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct    300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac    360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac    420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat    480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt    540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact    600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat    660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta    720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg    780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag    840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc    900
ttagacattg actatgaggg caatgtcact ttttcctgct ccgaaccaca gattgtgccc    960
atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat   1020
gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca   1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc   1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat   1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat   1260
gatgaagcag cacccccggc tccagacagc acttgggtgc agatttattc tggaaatagc   1320
tactattttg gagggtgccc cgacaatctc accgattccc aatgtttaaa tcccattaag   1380
gctttccaag gctgcatgag gctcatcttt attgataacc agcccaagga cctcatttca   1440
gttcagcaag gttccctggg gaattttagt gatttacaca ttgatctgtg tagcatcaaa   1500
gacaggtgtt tgccaaacta ctgtgaacat ggaggaagct gctcccagtc ctggactacc   1560
ttctattgta actgcagtga cacaagttac actggtgcca cctgccacaa ctccatctac   1620
gagcaatcct gcgaggtgta caggcaccag gggaatacag ccggcttctt ctacatcgac   1680
tcagatggca gcggcccact gggacctctc caggtgtact gcaatatcac tgaggacaag   1740
atctggacat cagtgcagca caacaataca gagctgaccc gagtgcgggg cgctaacccct   1800
gagaagccct atgccatggc cttggactac gggggcagca tggaacagct ggaggccgtg   1860
atcgacggct ctgagcactg tgagcaggag gtggcctacc actgcaggag gtcccgcctg   1920
ctcaacacgc cggatggaac accatttacc tggtggattg ggcggtccaa tgaaaggcac   1980
ccttactggg gaggttcccc tcctggggtc cagcagtgtg agtgtggcct agacgagagc   2040
tgcctggaca ttcagcactt ttgcaattgc gacgctgaca aggatgaatg gacaaatgat   2100
actggctttc tttccttcaa agaccacttg cctgtcactc agatagttat cactgatacc   2160
gacagatcaa actcagaagc cgcttggaga attggtccct tgcgttgcta tggtgaccgt   2220
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25

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gagtacaaaa tcgaaagaag ctttctctct gcattacatg agcacaagat gttcttactc   2280
ccttatccct tttccctgca gtgtgcccta gtcttgaaaa ttatccacat gtccagtgct   2340
ttcccatacc ccactgaaaa cgataaacca tgttga                            2376


<210> 22
<211> 791
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(791)
<223> Xaa = Any Amino Acid


<400> 22
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 1               5                  10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
 65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
        195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
        275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305                 310                 315                 320
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
```

26

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                           325                      330                      335
    Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
                       340                      345                      350
    Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                   355                      360                      365
    Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
               370                      375                      380
    Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
    385                      390                      395                      400
    Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                       405                      410                      415
    Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                   420                      425                      430
    Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
               435                      440                      445
    Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
           450                      455                      460
    Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
    465                      470                      475                      480
    Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                       485                      490                      495
    Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
                   500                      505                      510
    Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
               515                      520                      525
    Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
       530                      535                      540
    Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
    545                      550                      555                      560
    Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                       565                      570                      575
    Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
                   580                      585                      590
    Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
               595                      600                      605
    Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
           610                      615                      620
    Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
    625                      630                      635                      640
    Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                   645                      650                      655
    Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
               660                      665                      670
    Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
           675                      680                      685
    Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
       690                      695                      700
    Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
    705                      710                      715                      720
    Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
                   725                      730                      735
    Tyr Gly Asp Arg Glu Tyr Lys Ile Glu Arg Ser Phe Leu Ser Ala Leu
               740                      745                      750
    His Glu His Lys Met Phe Leu Leu Pro Tyr Pro Phe Ser Leu Gln Cys
           755                      760                      765
    Ala Leu Val Leu Lys Ile Ile His Met Ser Ser Ala Phe Pro Tyr Pro
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27

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     770                    775                    780
Thr Glu Asn Asp Lys Pro Cys
785                    790


<210> 23
<211> 3897
<212> DNA
<213> Homo sapiens


<400> 23
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tgtgatgatc cactagcatc cctgctctct ccaatggctt tttccagttc ctcagacctc     120
actggcactc acagcccagc tcaactcaac tggagagttg gaactggcgg ttggtcccca     180
gcagattcca atgctcaaca gtggctccag atggacctgg gaaacagagt agagattaca     240
gcagtggcca cgcagggaag atacggaagc tctgactggg tgacgagtta cagcctgatg     300
ttcagtgaca caggacgcaa ctggaaacag tacaaacaag aagacagcat ctggaccttt     360
gcaggaaaca tgaatgctga cagcgtggtg caccacaagc tattgcactc agtgagagcc     420
cgatttgttc gctttgtgcc cctggaatgg aatcccagtg ggaagattgg catgagagtc     480
gaggtctacg gatgttccta taaatcagac gttgctgact ttgatggccg aagctcactt     540
ctgtacaggt tcaatcagaa gttgatgagt actctcaaag atgtgatctc cctgaagttc     600
aagagcatgc aaggagatgg ggtcctgttc catggagaag gtcagcgtgg agaccacatc     660
accttggaac tccagaaggg gaggctcgcc ctacacctca atttgggtga cagcaaagcg     720
cggctcagca gcagcttgcc ctctgccacc ctgggcagcc tcctggatga ccagcactgg     780
cactcggtcc tcattgagcg ggtgggcaag caggtgaact tcacggtgga caagcacaca     840
cagcacttcc gcaccaaggg cgagacggat gccttagaca ttgactatga gcttagtttt     900
ggaggaattc cagtaccagg aaaacctggg accttttaa agaaaaactt ccatggatgc     960
atcgaaaacc tttactacaa tggagtaaac ataattgacc tggctaagag acgaaagcat    1020
cagatctata ctgtgggcaa tgtcactttt tcctgctccg aaccacagat tgtgcccatc    1080
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ctctcagtga gtttccagtt tcgaacatgg aacaaggatg gtctgcttct gtccacagag    1200
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gaagcagcac ccccggctcc agacagcact tgggtgcaga tttattctgg aaatagctac    1440
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ttccaaggct gcatgaggct catctttatt gataaccagc ccaaggacct catttcagtt    1560
cagcaaggtt ccctggggga ttttagtgat ttacacattg atctgtgtag catcaaagac    1620
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tattgtaact gcagtgacac aagttacact ggtgccacct gccacaactc catctacgag    1740
caatcctgcg aggtgtacag gcaccagggg aatacagccg gcttcttcta catcgactca    1800
gatggcagcg gcccactggg acctctccag gtgtactgca atatcactga ggacaagatc    1860
tggacatcag tgcagcacaa caatacagag ctgacccgag tgcggggcgc taaccctgag    1920
aagccctatg ccatggcctt ggactacggg ggcagcatgg aacagctgga ggccgtgatc    1980
gacggctctg agcactgtga gcaggaggtg gcctaccact gcaggaggtc ccgcctgctc    2040
aacacgccgg atggaacacc atttaccтgg tggattgggc ggtccaatga aaggcaccct    2100
tactggggag gttcccctcc tggggtccag cagtgtgagt gtggcctaga cgagagctgc    2160
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ctagaaaatc ttggcattaa agacttcatt cgactcgaaa taagctctcc ttcagagatc    2520
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ctgaatgaca accaatggca ctatgtccgg gctgagagga acctcaagga gacctccctg    2640
caggtggaca accttccaag gagcaccagg gagacgtcgg aggagggcca ttttcgactg    2700
cagctgaaca gccagttgtt tgtaggggga acgtcatcca gacagaaagg cttcctagga    2760
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28

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tgcattcgct ccttacactt gaatggacag aaaatggacc tggaagagag ggcaaaggtc    2820
acatctggag tcaggccagg ctgccccggc cactgcagca gctacggcag catctgccac    2880
aacggggggca agtgtgtgga gaagcacaat ggctacctgt gtgattgcac caattcacct    2940
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gcacccagtc ttttgctctt tatcaattct tcttctcagg acttcgtggt tgttctgctc    3180
tgcaagaatg gaagcttaca ggttcgctat cacctaaaca aggaagaaac ccatgtattc    3240
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ggaagagagc ttaccattca gatggaccag caacttcgac tcagttataa cttctctccg    3360
gaagtagagt tcagggttat aaggtcactc accttgggca aagtcacaga gaatcttggt    3420
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cagtacaacc acatagcacc actgaaggct gccctgcgcc atgccactgt cgcgcctgtg    3540
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ctcacaaatg ctgttcgaag tgattcggca gtcatcggag gggtgatagc agtggtgata    3720
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catcgtacga gccagatgaa ggagaaggaa tatccagaaa atttggacag ttccttcaga    3840
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<210> 24
<211> 1298
<212> PRT
<213> Homo sapiens

<400> 24

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Met Phe Leu Ala Asn Arg Ile Trp Ser Leu Ser Leu Cys Pro Pro Ile
1               5                   10                  15
Ile Ile Asp Asn Cys Asp Asp Pro Leu Ala Ser Leu Leu Ser Pro Met
            20                  25                  30
Ala Phe Ser Ser Ser Ser Asp Leu Thr Gly Thr His Ser Pro Ala Gln
        35                  40                  45
Leu Asn Trp Arg Val Gly Thr Gly Gly Trp Ser Pro Ala Asp Ser Asn
    50                  55                  60
Ala Gln Gln Trp Leu Gln Met Asp Leu Gly Asn Arg Val Glu Ile Thr
65                  70                  75                  80
Ala Val Ala Thr Gln Gly Arg Tyr Gly Ser Ser Asp Trp Val Thr Ser
                85                  90                  95
Tyr Ser Leu Met Phe Ser Asp Thr Gly Arg Asn Trp Lys Gln Tyr Lys
                100                 105                 110
Gln Glu Asp Ser Ile Trp Thr Phe Ala Gly Asn Met Asn Ala Asp Ser
        115                 120                 125
Val Val His His Lys Leu Leu His Ser Val Arg Ala Arg Phe Val Arg
    130                 135                 140
Phe Val Pro Leu Glu Trp Asn Pro Ser Gly Lys Ile Gly Met Arg Val
145                 150                 155                 160
Glu Val Tyr Gly Cys Ser Tyr Lys Ser Asp Val Ala Asp Phe Asp Gly
                165                 170                 175
Arg Ser Ser Leu Leu Tyr Arg Phe Asn Gln Lys Leu Met Ser Thr Leu
                180                 185                 190
Lys Asp Val Ile Ser Leu Lys Phe Lys Ser Met Gln Gly Asp Gly Val
        195                 200                 205
Leu Phe His Gly Glu Gly Gln Arg Gly Asp His Ile Thr Leu Glu Leu
    210                 215                 220
Gln Lys Gly Arg Leu Ala Leu His Leu Asn Leu Gly Asp Ser Lys Ala
225                 230                 235                 240
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29

Arg Leu Ser Ser Ser Leu Pro Ser Ala Thr Leu Gly Ser Leu Leu Asp
                245   250   255
Asp Gln His Trp His Ser Val Leu Ile Glu Arg Val Gly Lys Gln Val
            260   265   270
Asn Phe Thr Val Asp Lys His Thr Gln His Phe Arg Thr Lys Gly Glu
        275   280   285
Thr Asp Ala Leu Asp Ile Asp Tyr Glu Leu Ser Phe Gly Gly Ile Pro
    290   295   300
Val Pro Gly Lys Pro Gly Thr Phe Leu Lys Lys Asn Phe His Gly Cys
305   310   315   320
Ile Glu Asn Leu Tyr Tyr Asn Gly Val Asn Ile Ile Asp Leu Ala Lys
                325   330   335
Arg Arg Lys His Gln Ile Tyr Thr Val Gly Asn Val Thr Phe Ser Cys
            340   345   350
Ser Glu Pro Gln Ile Val Pro Ile Thr Phe Val Asn Ser Ser Gly Ser
        355   360   365
Tyr Leu Leu Leu Pro Gly Thr Pro Gln Ile Asp Gly Leu Ser Val Ser
    370   375   380
Phe Gln Phe Arg Thr Trp Asn Lys Asp Gly Leu Leu Leu Ser Thr Glu
385   390   395   400
Leu Ser Glu Gly Ser Gly Thr Leu Leu Leu Ser Leu Glu Gly Gly Ile
                405   410   415
Leu Arg Leu Val Ile Gln Lys Met Thr Glu Arg Val Ala Glu Ile Leu
            420   425   430
Thr Gly Ser Asn Leu Asn Asp Gly Leu Trp His Ser Val Ser Ile Asn
        435   440   445
Ala Arg Arg Asn Arg Ile Thr Leu Thr Leu Asp Asp Glu Ala Ala Pro
    450   455   460
Pro Ala Pro Asp Ser Thr Trp Val Gln Ile Tyr Ser Gly Asn Ser Tyr
465   470   475   480
Tyr Phe Gly Gly Cys Pro Asp Asn Leu Thr Asp Ser Gln Cys Leu Asn
                485   490   495
Pro Ile Lys Ala Phe Gln Gly Cys Met Arg Leu Ile Phe Ile Asp Asn
            500   505   510
Gln Pro Lys Asp Leu Ile Ser Val Gln Gln Gly Ser Leu Gly Asn Phe
        515   520   525
Ser Asp Leu His Ile Asp Leu Cys Ser Ile Lys Asp Arg Cys Leu Pro
    530   535   540
Asn Tyr Cys Glu His Gly Gly Ser Cys Ser Gln Ser Trp Thr Thr Phe
545   550   555   560
Tyr Cys Asn Cys Ser Asp Thr Ser Tyr Thr Gly Ala Thr Cys His Asn
                565   570   575
Ser Ile Tyr Glu Gln Ser Cys Glu Val Tyr Arg His Gln Gly Asn Thr
            580   585   590
Ala Gly Phe Phe Tyr Ile Asp Ser Asp Gly Ser Gly Pro Leu Gly Pro
        595   600   605
Leu Gln Val Tyr Cys Asn Ile Thr Glu Asp Lys Ile Trp Thr Ser Val
    610   615   620
Gln His Asn Asn Thr Glu Leu Thr Arg Val Arg Gly Ala Asn Pro Glu
625   630   635   640
Lys Pro Tyr Ala Met Ala Leu Asp Tyr Gly Gly Ser Met Glu Gln Leu
                645   650   655
Glu Ala Val Ile Asp Gly Ser Glu His Cys Glu Gln Glu Val Ala Tyr
            660   665   670
His Cys Arg Arg Ser Arg Leu Leu Asn Thr Pro Asp Gly Thr Pro Phe
        675   680   685

30

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Thr Trp Trp Ile Gly Arg Ser Asn Glu Arg His Pro Tyr Trp Gly Gly
    690                     695                 700
Ser Pro Pro Gly Val Gln Gln Cys Glu Cys Gly Leu Asp Glu Ser Cys
705                     710                 715                 720
Leu Asp Ile Gln His Phe Cys Asn Cys Asp Ala Asp Lys Asp Glu Trp
                    725                 730                 735
Thr Asn Asp Thr Gly Phe Leu Ser Phe Lys Asp His Leu Pro Val Thr
                740                 745                 750
Gln Ile Val Ile Thr Asp Thr Asp Arg Ser Asn Ser Glu Ala Ala Trp
            755                 760                 765
Arg Ile Gly Pro Leu Arg Cys Tyr Gly Asp Arg Arg Phe Trp Asn Ala
    770                 775                 780
Val Ser Phe Tyr Thr Glu Ala Ser Tyr Leu His Phe Pro Thr Phe His
785                 790                 795                 800
Ala Glu Phe Ser Ala Asp Ile Ser Phe Phe Phe Lys Thr Thr Ala Leu
                805                 810                 815
Ser Gly Val Phe Leu Glu Asn Leu Gly Ile Lys Asp Phe Ile Arg Leu
                820                 825                 830
Glu Ile Ser Ser Pro Ser Glu Ile Thr Phe Ala Ile Asp Val Gly Asn
            835                 840                 845
Gly Pro Val Glu Leu Val Val Gln Ser Pro Ser Leu Leu Asn Asp Asn
    850                 855                 860
Gln Trp His Tyr Val Arg Ala Glu Arg Asn Leu Lys Glu Thr Ser Leu
865                 870                 875                 880
Gln Val Asp Asn Leu Pro Arg Ser Thr Arg Glu Thr Ser Glu Glu Gly
                885                 890                 895
His Phe Arg Leu Gln Leu Asn Ser Gln Leu Phe Val Gly Gly Thr Ser
            900                 905                 910
Ser Arg Gln Lys Gly Phe Leu Gly Cys Ile Arg Ser Leu His Leu Asn
        915                 920                 925
Gly Gln Lys Met Asp Leu Glu Glu Arg Ala Lys Val Thr Ser Gly Val
    930                 935                 940
Arg Pro Gly Cys Pro Gly His Cys Ser Ser Tyr Gly Ser Ile Cys His
945                 950                 955                 960
Asn Gly Gly Lys Cys Val Glu Lys His Asn Gly Tyr Leu Cys Asp Cys
                965                 970                 975
Thr Asn Ser Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val Ser Ala
                980                 985                 990
Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu Pro Tyr
            995                 1000                1005
Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr Thr Asp
    1010                1015                1020
Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr Thr Gln
1025                1030                1035                1040
Ala Pro Ser Leu Leu Leu Phe Ile Asn Ser Ser Ser Gln Asp Phe Val
                1045                1050                1055
Val Val Leu Leu Cys Lys Asn Gly Ser Leu Gln Val Arg Tyr His Leu
                1060                1065                1070
Asn Lys Glu Glu Thr His Val Phe Thr Ile Asp Ala Asp Asn Phe Ala
            1075                1080                1085
Asn Arg Arg Met His His Leu Lys Ile Asn Arg Glu Gly Arg Glu Leu
    1090                1095                1100
Thr Ile Gln Met Asp Gln Gln Leu Arg Leu Ser Tyr Asn Phe Ser Pro
1105                1110                1115                1120
Glu Val Glu Phe Arg Val Ile Arg Ser Leu Thr Leu Gly Lys Val Thr
                1125                1130                1135
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31

```
Glu Asn Leu Gly Leu Asp Ser Glu Val Ala Lys Ala Asn Ala Met Gly
            1140                    1145                1150
Phe Ala Gly Cys Met Ser Ser Val Gln Tyr Asn His Ile Ala Pro Leu
        1155                    1160            1165
Lys Ala Ala Leu Arg His Ala Thr Val Ala Pro Val Thr Val His Gly
    1170                    1175                1180
Thr Leu Thr Glu Ser Ser Cys Gly Phe Met Val Asp Ser Asp Val Asn
1185                    1190            1195                1200
Ala Val Thr Thr Val His Ser Ser Ser Asp Pro Phe Gly Lys Thr Asp
                1205                    1210                1215
Glu Arg Glu Pro Leu Thr Asn Ala Val Arg Ser Asp Ser Ala Val Ile
            1220                    1225            1230
Gly Gly Val Ile Ala Val Val Ile Phe Ile Ile Phe Cys Ile Ile Gly
        1235                    1240            1245
Ile Met Thr Arg Phe Leu Tyr Gln His Lys Gln Ser His Arg Thr Ser
    1250                    1255            1260
Gln Met Lys Glu Lys Glu Tyr Pro Glu Asn Leu Asp Ser Ser Phe Arg
1265                    1270            1275                1280
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Phe Ile
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<210> 25
<211> 3528
<212> DNA
<213> Homo sapiens

<400> 25

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ggatgttcct ataaatcaga cgttgctgac tttgatggcc gaagctcact tctgtacagg   180
ttcaatcaga agttgatgag tactctcaaa gatgtgatct ccctgaagtt caagagcatg   240
caaggagatg gggtcctgtt ccatggagaa ggtcagcgtg gagaccacat caccttggaa   300
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ctcattgagc gggtgggcaa gcaggtgaac ttcacggtgg acaagcacac acagcacttc   480
cgcaccaagg gcgagacgga tgccttagac attgactatg agcttagttt tggaggaatt   540
ccagtaccag gaaaacctgg gaccttttta aagaaaaact tccatggatg catcgaaaac   600
ctttactaca atggagtaaa cataattgac ctggctaaga gacgaaagca tcagatctat   660
actgtgggca atgtcacttt ttcctgctcc gaaccacaga ttgtgcccat cacatttgtc   720
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tgcagtgaca caagttacac tggtgccacc tgccacaact ccatctacga gcaatcctgc  1380
gaggtgtaca ggcaccaggg gaatacagcc ggcttcttct acatcgactc agatggcagc  1440
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gtgcagcaca acaatacaga gctgacccga gtgcggggcg ctaaccctga gaagccctat  1560
gccatggcct tggactacgg gggcagcatg gaacagctgg aggccgtgat cgacggctct  1620
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                                    32
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cttggcatta aagacttcat tcgactcgaa ataagctctc cttcagagat cacctttgcc    2160
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aagtgtgtgg agaagcacaa tggctacctg tgtgattgca ccaattcacc ttatgaaggg    2580
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<210> 26
<211> 1175
<212> PRT
<213> Homo sapiens

<400> 26
Met Asn Ala Asp Ser Val Val His His Lys Leu Leu His Ser Val Arg
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Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn Pro Ser Gly Lys
            20   25   30
Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr Lys Ser Asp Val
        35   40   45
Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg Phe Asn Gln Lys
    50   55   60
Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys Phe Lys Ser Met
65   70   75   80
Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln Arg Gly Asp His
                85   90   95
Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu His Leu Asn Leu
            100   105   110
Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro Ser Ala Thr Leu
        115   120   125
Gly Ser Leu Leu Asp Asp Gln His Trp His Ser Val Leu Ile Glu Arg
```

33
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```
              130                   135                   140
Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His Thr Gln His Phe
145                   150                   155                   160
Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp Tyr Glu Leu Ser
                  165                   170                   175
Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr Phe Leu Lys Lys
                  180                   185                   190
Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn Gly Val Asn Ile
              195                   200                   205
Ile Asp Leu Ala Lys Arg Arg Lys His Gln Ile Tyr Thr Val Gly Asn
          210                   215                   220
Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro Ile Thr Phe Val
225                   230                   235                   240
Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr Pro Gln Ile Asp
                  245                   250                   255
Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn Lys Asp Gly Leu
                  260                   265                   270
Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr Leu Leu Leu Ser
              275                   280                   285
Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys Met Thr Glu Arg
      290                   295                   300
Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp Gly Leu Trp His
305                   310                   315                   320
Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr Leu Thr Leu Asp
                  325                   330                   335
Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp Val Gln Ile Tyr
              340                   345                   350
Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp Asn Leu Thr Asp
          355                   360                   365
Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly Cys Met Arg Leu
      370                   375                   380
Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser Val Gln Gln Gly
385                   390                   395                   400
Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu Cys Ser Ile Lys
                  405                   410                   415
Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly Ser Cys Ser Gln
                  420                   425                   430
Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr Ser Tyr Thr Gly
          435                   440                   445
Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys Glu Val Tyr Arg
      450                   455                   460
His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp Ser Asp Gly Ser
465                   470                   475                   480
Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile Thr Glu Asp Lys
                  485                   490                   495
Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu Thr Arg Val Arg
                  500                   505                   510
Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu Asp Tyr Gly Gly
          515                   520                   525
Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser Glu His Cys Glu
      530                   535                   540
Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu Leu Asn Thr Pro
545                   550                   555                   560
Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser Asn Glu Arg His
                  565                   570                   575
Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln Cys Glu Cys Gly
```

34

```
                     580                          585                          590
     Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys Asn Cys Asp Ala
             595                          600                      605
     Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu Ser Phe Lys Asp
         610                          615                      620
     His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr Asp Arg Ser Asn
     625                          630                      635                  640
     Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys Tyr Gly Asp Arg
                     645                          650                      655
     Arg Phe Trp Asn Ala Val Ser Phe Tyr Thr Glu Ala Ser Tyr Leu His
                 660                          665                      670
     Phe Pro Thr Phe His Ala Glu Phe Ser Ala Asp Ile Ser Phe Phe Phe
             675                          680                      685
     Lys Thr Thr Ala Leu Ser Gly Val Phe Leu Glu Asn Leu Gly Ile Lys
         690                          695                      700
     Asp Phe Ile Arg Leu Glu Ile Ser Ser Pro Ser Glu Ile Thr Phe Ala
     705                          710                      715                  720
     Ile Asp Val Gly Asn Gly Pro Val Glu Leu Val Val Gln Ser Pro Ser
                     725                          730                      735
     Leu Leu Asn Asp Asn Gln Trp His Tyr Val Arg Ala Glu Arg Asn Leu
                 740                          745                      750
     Lys Glu Thr Ser Leu Gln Val Asp Asn Leu Pro Arg Ser Thr Arg Glu
             755                          760                      765
     Thr Ser Glu Glu Gly His Phe Arg Leu Gln Leu Asn Ser Gln Leu Phe
         770                          775                      780
     Val Gly Gly Thr Ser Ser Arg Gln Lys Gly Phe Leu Gly Cys Ile Arg
     785                          790                      795                  800
     Ser Leu His Leu Asn Gly Gln Lys Met Asp Leu Glu Glu Arg Ala Lys
                     805                          810                      815
     Val Thr Ser Gly Val Arg Pro Gly Cys Pro Gly His Cys Ser Ser Tyr
                 820                          825                      830
     Gly Ser Ile Cys His Asn Gly Gly Lys Cys Val Glu Lys His Asn Gly
             835                          840                      845
     Tyr Leu Cys Asp Cys Thr Asn Ser Pro Tyr Glu Gly Pro Phe Cys Lys
         850                          855                      860
     Lys Glu Val Ser Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met
     865                          870                      875                  880
     Phe Gln Glu Pro Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser
                     885                          890                      895
     Ala Ile Tyr Thr Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser
                 900                          905                      910
     Phe Val Thr Thr Gln Ala Pro Ser Leu Leu Leu Phe Ile Asn Ser Ser
             915                          920                      925
     Ser Gln Asp Phe Val Val Val Leu Leu Cys Lys Asn Gly Ser Leu Gln
         930                          935                      940
     Val Arg Tyr His Leu Asn Lys Glu Glu Thr His Val Phe Thr Ile Asp
     945                          950                      955                  960
     Ala Asp Asn Phe Ala Asn Arg Arg Met His His Leu Lys Ile Asn Arg
                     965                          970                      975
     Glu Gly Arg Glu Leu Thr Ile Gln Met Asp Gln Gln Leu Arg Leu Ser
                 980                          985                      990
     Tyr Asn Phe Ser Pro Glu Val Glu Phe Arg Val Ile Arg Ser Leu Thr
             995                          1000                     1005
     Leu Gly Lys Val Thr Glu Asn Leu Gly Leu Asp Ser Glu Val Ala Lys
         1010                         1015                     1020
     Ala Asn Ala Met Gly Phe Ala Gly Cys Met Ser Ser Val Gln Tyr Asn
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35

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     1025                    1030                  1035                        1040
His Ile Ala Pro Leu Lys Ala Ala Leu Arg His Ala Thr Val Ala Pro
                      1045                  1050                  1055
Val Thr Val His Gly Thr Leu Thr Glu Ser Ser Cys Gly Phe Met Val
                1060                  1065                  1070
Asp Ser Asp Val Asn Ala Val Thr Thr Val His Ser Ser Ser Asp Pro
          1075                  1080                  1085
Phe Gly Lys Thr Asp Glu Arg Glu Pro Leu Thr Asn Ala Val Arg Ser
      1090                  1095                  1100
Asp Ser Ala Val Ile Gly Gly Val Ile Ala Val Val Ile Phe Ile Ile
1105                  1110                  1115                        1120
Phe Cys Ile Ile Gly Ile Met Thr Arg Phe Leu Tyr Gln His Lys Gln
                1125                  1130                  1135
Ser His Arg Thr Ser Gln Met Lys Glu Lys Glu Tyr Pro Glu Asn Leu
          1140                  1145                  1150
Asp Ser Ser Phe Arg Asn Glu Ile Asp Leu Gln Asn Thr Val Ser Glu
      1155                  1160                  1165
Cys Lys Arg Glu Tyr Phe Ile
      1170                  1175
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<210> 27
<211> 4869
<212> DNA
<213> Homo sapiens

<400> 27

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36

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ᵢatcgacggct ctgagcactg tgagcaggag gtggcctacc actgcaggag gtcccgcctg   1920
  ctcaacacgc cggatggaac accatttacc tggtggattg ggcggtccaa tgaaaggcac   1980
ᵖccttactggg gaggttcccc tcctggggtc cagcagtgtg agtgtggcct agacgagagc   2040
ᵗtgcctggaca ttcagcactt ttgcaattgc gacgctgaca aggatgaatg gacaaatgat   2100
ᵃactggctttc tttccttcaa agaccacttg cctgtcactc agatagttat cactgatacc   2160
ᵍgacagatcaa actcagaagc cgcttggaga attggtccct tgcgttgcta tggtgaccga   2220
ᵉcgcttctgga acgccgtctc attttataca gaagcctctt acctccactt tcctaccttc   2280
ᵉcatgcggaat tcagtgccga tatttccttc ttttttaaaa ccacagcatt atccggagtt   2340
ᵗttcctagaaa atcttggcat taaagacttc attcgactcg aaataagctc tccttcagag   2400
  atcacctttg ccatcgatgt tgggaatggt cctgtggagc ttgtagtcca gtctccttct   2460
  cttctgaatg acaaccaatg gcactatgtc cgggctgaga ggaacctcaa ggagacctcc   2520
  ctgcaggtgg acaaccttcc aaggagcacc agggagacgt cggaggaggg ccattttcga   2580
  ctgcagctga acagccagtt gtttgtaggg ggaacgtcat ccagacagaa aggcttccta   2640
  ggatgcattc gctccttaca cttgaatgga cagaaaatgg acctggaaga gagggcaaag   2700
  gtcacatctg gagtcaggcc aggctgcccc ggccactgca gcagctacgg cagcatctgc   2760
  cacaacgggg gcaagtgtgt ggagaagcac aatggctacc tgtgtgattg caccaattca   2820
  ccttatgaag ggcccttttg caaaaaagag gtttctgctg tttttgaggc tggcacgtcg   2880
  gttacttaca tgtttcaaga accctatcct gtgaccaaga atataagcct ctcatcctca   2940
  gctatttaca cagattcagc tccatccaag gaaaacattg cacttagctt tgtgacaacc   3000
  caggcaccca gtcttttgct ctttatcaat tcttcttctc aggacttcgt ggttgttctg   3060
  ctctgcaaga atggaagctt acaggttcgc tatcacctaa acaaggaaga aacccatgta   3120
  ttcaccattg atgcagataa ctttgctaac agaaggatgc accacttgaa gattaaccga   3180
  gagggaagag agcttaccat tcagatggac cagcaacttc gactcagtta taacttctct   3240
  ccggaagtag agttcagggt tataaggtca ctccacttgg gcaaagtcac agagaatctt   3300
  ggtttggatt ctgaagttgc taaagcaaat gccatgggtt ttgctggatg catgtcttcc   3360
  gtccagtaca accacatagc accactgaag gctgccctgc gccatgccac tgtcgcgcct   3420
  gtgactgtcc atgggacctt gacggaatcc agctgtggct tcatggtgga ctcagatgtg   3480
  aatgcagtga ccacggtgca ttcttcatca gatccttttg ggaagacaga tgagcgggaa   3540
  ccactcacaa atgctgttcg aagtgattcg gcagtcatcg gagggtgat agcagtggtg   3600
  atattcatca tcttctgtat catcggcatc atgacccggt tcctctacca gcacaagcag   3660
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tcacatcgta cgagccagat gaaggagaag gaatatccag aaaatttgga cagttccttc    3720
agaaatgaaa ttgacttgca aaacacagtg agcgagtgta acgggaata tttcatctga      3780
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<210> 4
<211> 1259
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(1259)
<223> Xaa = Any Amino Acid

<400> 4
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Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1               5                  10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
        195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
        275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305                 310                 315                 320
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
                325                 330                 335
```

Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
            340   345   350
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
            355   360   365
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
    370   375   380
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
385   390   395   400
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                405   410   415
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                420   425   430
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
            435   440   445
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
    450   455   460
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
465   470   475   480
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                485   490   495
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
                500   505   510
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
            515   520   525
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
    530   535   540
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
545   550   555   560
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                565   570   575
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
                580   585   590
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
            595   600   605
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
    610   615   620
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
625   630   635   640
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                645   650   655
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
                660   665   670
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
            675   680   685
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
    690   695   700
Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
705   710   715   720
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
                725   730   735
Tyr Gly Asp Arg Arg Phe Trp Asn Ala Val Ser Phe Tyr Thr Glu Ala
            740   745   750
Ser Tyr Leu His Phe Pro Thr Phe His Ala Glu Phe Ser Ala Asp Ile
            755   760   765
Ser Phe Phe Phe Lys Thr Thr Ala Leu Ser Gly Val Phe Leu Glu Asn
    770   775   780

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Leu Gly Ile Lys Asp Phe Ile Arg Leu Glu Ile Ser Ser Pro Ser Glu
785                 790                 795                 800
Ile Thr Phe Ala Ile Asp Val Gly Asn Gly Pro Val Glu Leu Val Val
                805                 810                 815
Gln Ser Pro Ser Leu Leu Asn Asp Asn Gln Trp His Tyr Val Arg Ala
                820                 825                 830
Glu Arg Asn Leu Lys Glu Thr Ser Leu Gln Val Asp Asn Leu Pro Arg
            835                 840                 845
Ser Thr Arg Glu Thr Ser Glu Glu Gly His Phe Arg Leu Gln Leu Asn
        850                 855                 860
Ser Gln Leu Phe Val Gly Gly Thr Ser Ser Arg Gln Lys Gly Phe Leu
865                 870                 875                 880
Gly Cys Ile Arg Ser Leu His Leu Asn Gly Gln Lys Met Asp Leu Glu
                885                 890                 895
Glu Arg Ala Lys Val Thr Ser Gly Val Arg Pro Gly Cys Pro Gly His
                900                 905                 910
Cys Ser Ser Tyr Gly Ser Ile Cys His Asn Gly Gly Lys Cys Val Glu
            915                 920                 925
Lys His Asn Gly Tyr Leu Cys Asp Cys Thr Asn Ser Pro Tyr Glu Gly
    930                 935                 940
Pro Phe Cys Lys Lys Glu Val Ser Ala Val Phe Glu Ala Gly Thr Ser
945                 950                 955                 960
Val Thr Tyr Met Phe Gln Glu Pro Tyr Pro Val Thr Lys Asn Ile Ser
                965                 970                 975
Leu Ser Ser Ser Ala Ile Tyr Thr Asp Ser Ala Pro Ser Lys Glu Asn
            980                 985                 990
Ile Ala Leu Ser Phe Val Thr Thr Gln Ala Pro Ser Leu Leu Leu Phe
            995                 1000                1005
Ile Asn Ser Ser Ser Gln Asp Phe Val Val Val Leu Leu Cys Lys Asn
    1010                1015                1020
Gly Ser Leu Gln Val Arg Tyr His Leu Asn Lys Glu Glu Thr His Val
1025                1030                1035                1040
Phe Thr Ile Asp Ala Asp Asn Phe Ala Asn Arg Arg Met His His Leu
                1045                1050                1055
Lys Ile Asn Arg Glu Gly Arg Glu Leu Thr Ile Gln Met Asp Gln Gln
            1060                1065                1070
Leu Arg Leu Ser Tyr Asn Phe Ser Pro Glu Val Glu Phe Arg Val Ile
        1075                1080                1085
Arg Ser Leu Thr Leu Gly Lys Val Thr Glu Asn Leu Gly Leu Asp Ser
    1090                1095                1100
Glu Val Ala Lys Ala Asn Ala Met Gly Phe Ala Gly Cys Met Ser Ser
1105                1110                1115                1120
Val Gln Tyr Asn His Ile Ala Pro Leu Lys Ala Ala Leu Arg His Ala
                1125                1130                1135
Thr Val Ala Pro Val Thr Val His Gly Thr Leu Thr Glu Ser Ser Cys
            1140                1145                1150
Gly Phe Met Val Asp Ser Asp Val Asn Ala Val Thr Thr Val His Ser
        1155                1160                1165
Ser Ser Asp Pro Phe Gly Lys Thr Asp Glu Arg Glu Pro Leu Thr Asn
    1170                1175                1180
Ala Val Arg Ser Asp Ser Ala Val Ile Gly Gly Val Ile Ala Val Val
1185                1190                1195                1200
Ile Phe Ile Ile Phe Cys Ile Ile Gly Ile Met Thr Arg Phe Leu Tyr
                1205                1210                1215
Gln His Lys Gln Ser His Arg Thr Ser Gln Met Lys Glu Lys Glu Tyr
            1220                1225                1230
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Pro Glu Asn Leu Asp Ser Ser Phe Arg Asn Glu Ile Asp Leu Gln Asn
        1235   1240   1245
Thr Val Ser Glu Cys Lys Arg Glu Tyr Phe Ile
    1250   1255

<210> 5
<211> 108
<212> DNA
<213> homo sapiens

<400> 5
atggattctt taccacggct gaccagcgtt ttgactttgc tgttctctgg cttgtggcat   60
ttaggattaa cagcgacaaa ctacctttgc aggaaacatg aatgctga   108

<210> 6
<211> 35
<212> PRT
<213> homo sapiens

<400> 6
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
1   5   10   15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Leu Cys Arg Lys
               20   25   30
His Glu Cys
          35

<210> 7
<211> 753
<212> DNA
<213> homo sapiens

<400> 7
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ttaggattaa cagcgacaaa ctacaactgt gatgatccac tagcatccct gctctctcca   120
atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg   180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg   240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct   300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac   360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac   420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat   480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt   540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact   600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag agatggggt cctgttccat   660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta   720
cacctcaatt tggtggtttg tagttctcct tga   753

<210> 8
<211> 250
<212> PRT
<213> homo sapiens

<400> 8
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1   5   10   15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp

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                    20                      25                      30
    Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35                      40                      45
    Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
        50                      55                      60
    Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
    65                      70                      75                      80
    Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                    85                      90                      95
    Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
                    100                     105                     110
    Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                     120                     125
    Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
        130                     135                     140
    His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
    145                     150                     155                     160
    Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                    165                     170                     175
    Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                    180                     185                     190
    Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                     200                     205
    Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
        210                     215                     220
    Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
    225                     230                     235                     240
    His Leu Asn Leu Val Val Cys Ser Ser Pro
                    245                     250

<210> 9
<211> 840
<212> DNA
<213> homo sapiens

<400> 9
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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct     300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac     360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac     420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt     540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact     600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag agatggggt cctgttccat     660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaagggag gctcgcccta     720
cacctcaatt tgggtgacag caaagcgcgg ctaagcactt gccctctgcc accctgggca     780
gcctcctgga tgaccagcac tggcactygg tcctcattga gcgggtgggc aagcaggtga     840

<210> 10
<211> 279
<212> PRT
<213> homo sapiens
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<220>
<221> VARIANT
<222> (1)...(279)
<223> Xaa = Any Amino Acid

<400> 10
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1   5   10   15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20   25   30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35   40   45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50   55   60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65   70   75   80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85   90   95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100   105   110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115   120   125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130   135   140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145   150   155   160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165   170   175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180   185   190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
        195   200   205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210   215   220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225   230   235   240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Thr Cys Pro Leu
                245   250   255
Pro Pro Trp Ala Ala Ser Trp Met Thr Ser Thr Gly Thr Xaa Ser Ser
            260   265   270
Leu Ser Gly Trp Ala Ser Arg
        275

<210> 11
<211> 1749
<212> DNA
<213> homo sapiens

<400> 11
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ttaggattaa cagcgacaaa ctacaactgt gatgatccac tagcatccct gctctctcca   120
atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg   180
agagttggaa ctggcggttg gtcccccagca gattccaatg ctcaacagtg gctccagatg   240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct   300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac   360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac   420

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cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat      480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt      540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact      600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat      660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta      720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg      780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag      840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc      900
ttagacattg actatgagct tagtttttgga ggaattccag taccaggaaa acctgggacc      960
tttttaaaga aaaacttcca tggatgcatc gaaaaccttt actacaatgg agtaaacata     1020
attraccttg ctaagagacg aaagcatcag atctatactg tgggcaatgt cacttttttcc     1080
tgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg     1140
ctgccggca ccccccaaat tgatgggctc tcagtgagtt ccagtttcg aacatggaac       1200
aaggatggtc tgcttctgtc cacagagctg tctgagggct cgggaaccct gctgctgagc     1260
ctggagggtg gaatcctgag actcgtgatt cagaaaatga cagaacgcgt agctgaaatc     1320
ctcacaggca gcaacttgaa tgatggcctg tggcactcgg ttagcatcaa cgccaggagg     1380
aaccgcatca cgctcactct ggatgatgaa gcagcacccc cggctccaga cagcacttgg     1440
gtgcagattt attctggaaa tagctactat tttggaggtg tttgccaaac tactgtgaac     1500
atggaggaag ctgctcccag tcctggacta ccttctattg taactgcagt gacacaagtt     1560
acactggtgc cacctgccac aactccatct acgagcaatc ctgcgaggtg tacaggcacc     1620
aggggaatac agccggcttc ttctacatcg actcagatgg cagcggccca ctgggacctc     1680
tccaggtgta ctgcaatatc actgaggaca agatctggac atcagtgcag cacaacaata     1740
cagagctga                                                            1749
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<210> 12

<211> 582

<212> PRT

<213> homo sapiens

<220>

<221> VARIANT

<222> (1)...(582)

<223> Xaa = Any Amino Acid

<400> 12

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
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                           165                     170                     175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                     185                     190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                     200                     205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
        210                     215                     220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                     230                     235                     240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                    245                     250                     255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                260                     265                     270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                     280                     285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
        290                     295                     300
Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
305                     310                     315                     320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
                    325                     330                     335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
                340                     345                     350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
                355                     360                     365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
        370                     375                     380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385                     390                     395                     400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                    405                     410                     415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
                420                     425                     430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
            435                     440                     445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
        450                     455                     460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465                     470                     475                     480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Val Cys Gln
                    485                     490                     495
Thr Thr Val Asn Met Glu Glu Ala Ala Pro Ser Pro Gly Leu Pro Ser
            500                     505                     510
Ile Val Thr Ala Val Thr Gln Val Thr Leu Val Pro Pro Ala Thr Thr
            515                     520                     525
Pro Ser Thr Ser Asn Pro Ala Arg Cys Thr Gly Thr Arg Gly Ile Gln
        530                     535                     540
Pro Ala Ser Ser Thr Ser Thr Gln Met Ala Ala Ala His Trp Asp Leu
545                     550                     555                     560
Ser Arg Cys Thr Ala Ile Ser Leu Arg Thr Arg Ser Gly His Gln Cys
                    565                     570                     575
Ser Thr Thr Ile Gln Ser
                580
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<210> 13
<211> 1605

<212> DNA
<213> homo sapiens

<400> 13

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agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg       240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct       300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac       360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac       420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat       480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt       540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact       600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat       660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta       720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg       780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag       840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc       900
ttagacattg actatgaggg caatgtcact ttttcctgct ccgaaccaca gattgtgccc       960
atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat      1020
gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca      1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc      1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat      1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat      1260
gatgaagcag caccccggc tccagacagc acttgggtgc agatttattc tggaaatagc      1320
tactattttg gaggtgtttg ccaaactact gtgaacatgg aggaagctgc tcccagtcct      1380
ggactacctt ctattgtaac tgcagtgaca caagttacac tggtgccacc tgccacaact      1440
ccatctacga gcaatcctgc gaggtgtaca ggcaccaggg gaatacagcc ggcttcttct      1500
acatcgactc agatggcagc ggcccactgg gacctctcca ggtgtactgc aatatcactg      1560
aggacaagat ctggacatca gtgcagcaca acaatacaga gctga                      1605
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<210> 14
<211> 534
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(534)
<223> Xaa = Any Amino Acid

<400> 14

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 1               5                   10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
```

```
                        100                     105                    110
    Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                     120                     125
    Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
        130                     135                     140
    His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
    145                     150                     155                     160
    Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                    165                     170                     175
    Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                    180                     185                     190
    Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                     200                     205
    Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
        210                     215                     220
    Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
    225                     230                     235                     240
    His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                    245                     250                     255
    Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                    260                     265                     270
    Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                     280                     285
    Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
        290                     295                     300
    Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
    305                     310                     315                     320
    Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
                    325                     330                     335
    Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
                    340                     345                     350
    Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
            355                     360                     365
    Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
        370                     375                     380
    Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
    385                     390                     395                     400
    Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                    405                     410                     415
    Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                    420                     425                     430
    Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Val Cys Gln
            435                     440                     445
    Thr Thr Val Asn Met Glu Glu Ala Ala Pro Ser Pro Gly Leu Pro Ser
        450                     455                     460
    Ile Val Thr Ala Val Thr Gln Val Thr Leu Val Pro Pro Ala Thr Thr
    465                     470                     475                     480
    Pro Ser Thr Ser Asn Pro Ala Arg Cys Thr Gly Thr Arg Gly Ile Gln
                    485                     490                     495
    Pro Ala Ser Ser Thr Ser Thr Gln Met Ala Ala Ala His Trp Asp Leu
                    500                     505                     510
    Ser Arg Cys Thr Ala Ile Ser Leu Arg Thr Arg Ser Gly His Gln Cys
            515                     520                     525
    Ser Thr Thr Ile Gln Ser
        530
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<210> 15
<211> 2238
<212> DNA
<213> homo sapiens

<400> 15

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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg       180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg       240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct       300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac       360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac       420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat       480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt       540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact       600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat       660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta       720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg       780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag       840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc       900
ttagacattg actatgagct tagttttgga ggaattccag taccaggaaa acctgggacc       960
tttttaaaga aaaacttcca tggatgcatc gaaaaccttt actacaatgg agtaaacata      1020
attracctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cactttttcc      1080
ttgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg      1140
ctgcccggca ccccccaaat tgatgggctc tcagtgagtt tccagtttcg aacatggaac      1200
aaggatggtc tgcttctgtc cacagagctg tctgagggct cgggaacect gctgctgagc      1260
ctggagggtg gaatcctgag actcgtgatt cagaaaatga cagaacgcgt agctgaaatc      1320
ctcacaggca gcaacttgaa tgatggcctg tggcactcgg ttagcatcaa cgccaggagg      1380
aaccgcatca cgctcactct ggatgatgaa gcagcacccc cggctccaga cagcacttgg      1440
gtgcagattt attctggaaa tagctactat tttggagggt gccccgacaa tctcaccgat      1500
tcccaatgtt taaatcccat taaggctttc caaggctgca tgaggctcat ctttattgat      1560
aaccagccca aggacctcat ttcagttcag caaggttccc tggggaattt tagtgattta      1620
cacattgatc tgtgtagcat caaagacagg tgtttgccaa actactgtga acatggagga      1680
agctgctccc agtcctggac taccttctat tgtaactgca gtgacacaag ttacactggt      1740
gccacctgcc acaactccat ctacgagcaa tcctgcgagg tgtacaggca ccagggaat       1800
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acccgagtgc ggggcgctaa ccctgagaag ccctatgcca tggccttgga ctacgggggc      1980
agcatggaac agctggaggc cgtgatcgac ggctctgagc actgtgagca ggaggtggcc      2040
taccactgca ggaggtcccg cctgctcaac acgccggatg gaacaccatt tacctggtgg      2100
attgggcggt ccaatgaaag gcacccttac tggggaggtt cccctcctgg ggtccagcag      2160
tgtgagtgtg gcctagacga gagctgcctg gacattcagc acttttgcaa ttgcgacgct      2220
gacaaggatg aatggtaa                                                    2238
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<210> 16
<211> 745
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(745)
<223> Xaa = Any Amino Acid

<400> 16

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
            85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
            165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
            245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
305                 310                 315                 320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
            325                 330                 335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
            340                 345                 350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
            355                 360                 365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
    370                 375                 380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385                 390                 395                 400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
            405                 410                 415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
            420                 425                 430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
            435                 440                 445
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Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
    450                 455                 460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465                 470                 475                 480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                485                 490                 495
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
                500                 505                 510
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
            515                 520                 525
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
    530                 535                 540
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
545                 550                 555                 560
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                565                 570                 575
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
                580                 585                 590
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
        595                 600                 605
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
    610                 615                 620
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
625                 630                 635                 640
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
                645                 650                 655
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
                660                 665                 670
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
            675                 680                 685
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
    690                 695                 700
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
705                 710                 715                 720
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                725                 730                 735
Asn Cys Asp Ala Asp Lys Asp Glu Trp
                740                 745


<210> 17
<211> 2094
<212> DNA
<213> homo sapiens


<400> 17
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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg       180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg       240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct       300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac       360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac       420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat       480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt       540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact       600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat       660
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cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg    780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag    840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga cacggatgcc    900
ttagacattg actatgaggg caatgtcact ttttcctgct ccgaaccaca gattgtgccc    960
atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat   1020
gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca   1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc   1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat   1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat   1260
gatgaagcag caccccggc tccagacagc acttgggtgc agatttattc tggaaatagc   1320
tactattttg gagggtgccc cgacaatctc accgattccc aatgtttaaa tcccattaag   1380
gctttccaag gctgcatgag gctcatcttt attgataacc agcccaagga cctcatttca   1440
gttcagcaag gttccctggg gaatttttagt gatttacaca ttgatctgtg tagcatcaaa   1500
gacaggtgtt tgccaaacta ctgtgaacat ggaggaagct gctcccagtc ctggactacc   1560
ttctattgta actgcagtga cacaagttac actggtgcca cctgccacaa ctccatctac   1620
gagcaatcct gcgaggtgta caggcaccag gggaatacag ccggcttctt ctacatcgac   1680
tcagatggca gcggcccact gggacctctc caggtgtact gcaatatcac tgaggacaag   1740
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ggagaagccct atgccatggc cttggactac gggggcagca tggaacagct ggaggccgtg   1860
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ctcaacacgc cggatggaac accatttacc tggtggattg ggcggtccaa tgaaaggcac   1980
ccttactggg gaggttcccc tcctggggtc cagcagtgtg agtgtggcct agacgagagc   2040
tgcctggaca ttcagcactt ttgcaattgc gacgctgaca aggatgaatg gtaa          2094
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<400> 18
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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20   25   30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35   40   45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50   55   60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65   70   75   80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85   90   95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100   105   110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115   120   125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130   135   140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145   150   155   160
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Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
            165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
            245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305                 310                 315                 320
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
            325                 330                 335
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
            340                 345                 350
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
            355                 360                 365
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
    370                 375                 380
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
385                 390                 395                 400
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
            405                 410                 415
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
            420                 425                 430
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
            435                 440                 445
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
    450                 455                 460
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
465                 470                 475                 480
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
            485                 490                 495
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
            500                 505                 510
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
            515                 520                 525
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
    530                 535                 540
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
545                 550                 555                 560
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
            565                 570                 575
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
            580                 585                 590
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
            595                 600                 605
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Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
    610                 615                 620
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
625                 630                 635                 640
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                645                 650                 655
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
                660                 665                 670
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
        675                 680                 685
Asn Cys Asp Ala Asp Lys Asp Glu Trp
    690                 695
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<210> 19
<211> 2520
<212> DNA
<213> homo sapiens

<400> 19

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atggctttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct     300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac     360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac     420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt     540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact     600
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ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta     720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg     780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag     840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc     900
ttagacattg actatgagct tagttttgga ggaattccag taccaggaaa acctgggacc     960
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attracctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cacttttttcc    1080
tgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg    1140
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aaggatggtc tgcttctgtc cacagagctg tctgagggct cgggaacccct gctgctgagc    1260
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aaccgcatca cgctcactct ggatgatgaa gcagcacccc cggctccaga cagcacttgg    1440
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tcccaatgtt taaatcccat taaggctttc caaggctgca tgaggctcat ctttattgat    1560
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agcatggaac agctggaggc cgtgatcgac ggctctgagc actgtgagca ggaggtggcc    2040
taccactgca ggaggtcccg cctgctcaac acgccggatg gaacaccatt tacctggtgg    2100
attgggcggt ccaatgaaag gcacccttac tggggaggtt cccctcctgg ggtccagcag    2160
tgtgagtgtg gcctagacga gagctgcctg gacattcagc acttttgcaa ttgcgacgct    2220
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gacaaggatg aatggacaaa tgatactggc tttctttcct tcaaagacca cttgcctgtc    2280
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cccttgcgtt gctatggtga ccgtgagtac aaaatcgaaa gaagctttct ctctgcatta    2400
catgagcaca agatgttctt actcccttat cccttttccc tgcagtgtgc cctagtcttg    2460
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<210> 20
<211> 839
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(839)
<223> Xaa = Any Amino Acid

<400> 20

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             20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
         35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
     50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
 65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                 85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
                100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
        130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
        210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
        290                 295                 300
Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
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Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
                    325   330   335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
              340   345   350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
        355   360   365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
    370   375   380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385   390   395   400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                    405   410   415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
              420   425   430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
        435   440   445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
    450   455   460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465   470   475   480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                    485   490   495
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
              500   505   510
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
        515   520   525
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
    530   535   540
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
545   550   555   560
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                    565   570   575
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
              580   585   590
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
        595   600   605
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
    610   615   620
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
625   630   635   640
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
                    645   650   655
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
              660   665   670
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
        675   680   685
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
    690   695   700
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
705   710   715   720
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                    725   730   735
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
              740   745   750
Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr

```
         755                   760                   765
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
    770                   775                   780
Tyr Gly Asp Arg Glu Tyr Lys Ile Glu Arg Ser Phe Leu Ser Ala Leu
785                   790                   795                   800
His Glu His Lys Met Phe Leu Leu Pro Tyr Pro Phe Ser Leu Gln Cys
                805                   810                   815
Ala Leu Val Leu Lys Ile Ile His Met Ser Ser Ala Phe Pro Tyr Pro
                820                   825                   830
Thr Glu Asn Asp Lys Pro Cys
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<210> 21
<211> 2376
<212> DNA
<213> homo sapiens

<400> 21

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agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg    240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct    300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac    360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac    420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat    480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt    540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact    600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat    660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaagggggag gctcgcccta    720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg    780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag    840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc    900
ttagacattg actatgaggg caatgtcact ttttcctgct ccgaaccaca gattgtgccc    960
atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat   1020
gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca   1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc   1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat   1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat   1260
gatgaagcag cacccccggc tccagacagc acttgggtgc agatttattc tggaaatagc   1320
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gttcagcaag gttccctggg gaatttttagt gatttacaca ttgatctgtg tagcatcaaa   1500
gacaggtgtt tgccaaacta ctgtgaacat ggaggaagct gctcccagtc ctggactacc   1560
ttctattgta actgcagtga cacaagttac actggtgcca cctgccacaa ctccatctac   1620
gagcaatcct gcgaggtgta caggcaccag gggaatacag ccggcttctt ctacatcgac   1680
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gagaagccct atgccatggc cttggactac gggggcagca tggaacagct ggaggccgtg   1860
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ccttactggg gaggttcccc tcctggggtc cagcagtgtg agtgtggcct agacgagagc   2040
tgcctggaca ttcagcactt ttgcaattgc gacgctgaca aggatgaatg gacaaatgat   2100
actggctttc tttccttcaa agaccacttg cctgtcactc agatagttat cactgatacc   2160
gacagatcaa actcagaagc cgcttggaga attggtccct gcgttgcta tggtgaccgt   2220
gagtacaaaa tcgaaagaag ctttctctct gcattacatg agcacaagat gttcttactc   2280
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ccttatccct tttccctgca gtgtgcccta gtcttgaaaa ttatccacat gtccagtgct     2340
ttcccatacc ccactgaaaa cgataaacca tgttga                               2376
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<210> 22
<211> 791
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(791)
<223> Xaa = Any Amino Acid

<400> 22
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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
 65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
                100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305                 310                 315                 320
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
                325                 330                 335
```

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Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
        340                     345                 350
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
        355                 360                 365
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
    370                 375                 380
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
385                 390                 395                 400
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                405                 410                 415
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                420                 425                 430
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
            435                 440                 445
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
        450                 455                 460
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
465                 470                 475                 480
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                485                 490                 495
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
            500                 505                 510
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
        515                 520                 525
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
    530                 535                 540
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
545                 550                 555                 560
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                565                 570                 575
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
                580                 585                 590
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
            595                 600                 605
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
    610                 615                 620
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
625                 630                 635                 640
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
            645                 650                 655
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
            660                 665                 670
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
        675                 680                 685
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
        690                 695                 700
Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
705                 710                 715                 720
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
            725                 730                 735
Tyr Gly Asp Arg Glu Tyr Lys Ile Glu Arg Ser Phe Leu Ser Ala Leu
            740                 745                 750
His Glu His Lys Met Phe Leu Leu Pro Tyr Pro Phe Ser Leu Gln Cys
        755                 760                 765
Ala Leu Val Leu Lys Ile Ile His Met Ser Ser Ala Phe Pro Tyr Pro
        770                 775                 780
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27/37

Thr Glu Asn Asp Lys Pro Cys
785   790

<210> 23
<211> 3897
<212> DNA
<213> Homo sapiens

<400> 23
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gcagtggcca cgcagggaag atacggaagc tctgactggg tgacgagtta cagcctgatg   300
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cactcggtcc tcattgagcg ggtgggcaag caggtgaact tcacggtgga caagcacaca   840
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gcggaattca gtgccgatat ttccttcttt tttaaaacca cagcattatc cggagttttc 2460
ctagaaaatc ttggcattaa agacttcatt cgactcgaaa taagctctcc ttcagagatc 2520
acctttgcca tcgatgttgg gaatggtcct gtggagcttg tagtccagtc tccttctctt 2580
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caggtggaca accttccaag gagcaccagg gagacgtcgg aggagggcca ttttcgactg 2700
cagctgaaca gccagttgtt tgtaggggga acgtcatcca gacagaaagg cttcctagga 2760
tgcattcgct ccttacactt gaatggacag aaaatggacc tggaagagag ggcaaaggtc 2820

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acatctggag tcaggccagg ctgccccggc cactgcagca gctacggcag catctgccac    2880
aacggggca  agtgtgtgga gaagcacaat ggctacctgt gtgattgcac caattcacct    2940
tatgaagggc cctttgcaa  aaaagaggtt tctgctgttt ttgaggctgg cacgtcggtt    3000
acttacatgt ttcaagaacc ctatcctgtg accaagaata taagcctctc atcctcagct    3060
atttacacag attcagctcc atccaaggaa aacattgcac ttagctttgt gacaacccag    3120
gcacccagtc ttttgctctt tatcaattct tcttctcagg acttcgtggt tgttctgctc    3180
tgcaagaatg gaagcttaca ggttcgctat cacctaaaca aggaagaaac ccatgtattc    3240
accattgatg cagataactt tgctaacaga aggatgcacc acttgaagat taaccgagag    3300
ggaagagagc ttaccattca gatggaccag caacttcgac tcagttataa cttctctccg    3360
gaagtagagt tcagggttat aaggtcactc accttgggca aagtcacaga gaatcttggt    3420
ttggattctg aagttgctaa agcaaatgcc atgggttttg ctggatgcat gtcttccgtc    3480
cagtacaacc acatagcacc actgaaggct gccctgcgcc atgccactgt cgcgcctgtg    3540
actgtccatg ggaccttgac ggaatccagc tgtggcttca tggtggactc agatgtgaat    3600
gcagtgacca cggtgcattc ttcatcagat cctttggga  agacagatga gcgggaacca    3660
ctcacaaatg ctgttcgaag tgattcggca gtcatcggag gggtgatagc agtggtgata    3720
ttcatcatct tctgtatcat cggcatcatg acccggttcc tctaccagca caagcagtca    3780
catcgtacga gccagatgaa ggagaaggaa tatccagaaa atttggacag ttccttcaga    3840
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```

```
<210> 24
<211> 1298
<212> PRT
<213> Homo sapiens

<400> 24
Met Phe Leu Ala Asn Arg Ile Trp Ser Leu Ser Leu Cys Pro Pro Ile
1               5                   10                  15
Ile Ile Asp Asn Cys Asp Asp Pro Leu Ala Ser Leu Leu Ser Pro Met
            20                  25                  30
Ala Phe Ser Ser Ser Ser Asp Leu Thr Gly Thr His Ser Pro Ala Gln
        35                  40                  45
Leu Asn Trp Arg Val Gly Thr Gly Gly Trp Ser Pro Ala Asp Ser Asn
    50                  55                  60
Ala Gln Gln Trp Leu Gln Met Asp Leu Gly Asn Arg Val Glu Ile Thr
65                  70                  75                  80
Ala Val Ala Thr Gln Gly Arg Tyr Gly Ser Ser Asp Trp Val Thr Ser
                85                  90                  95
Tyr Ser Leu Met Phe Ser Asp Thr Gly Arg Asn Trp Lys Gln Tyr Lys
                100                 105                 110
Gln Glu Asp Ser Ile Trp Thr Phe Ala Gly Asn Met Asn Ala Asp Ser
            115                 120                 125
Val Val His His Lys Leu Leu His Ser Val Arg Ala Arg Phe Val Arg
    130                 135                 140
Phe Val Pro Leu Glu Trp Asn Pro Ser Gly Lys Ile Gly Met Arg Val
145                 150                 155                 160
Glu Val Tyr Gly Cys Ser Tyr Lys Ser Asp Val Ala Asp Phe Asp Gly
                165                 170                 175
Arg Ser Ser Leu Leu Tyr Arg Phe Asn Gln Lys Leu Met Ser Thr Leu
                180                 185                 190
Lys Asp Val Ile Ser Leu Lys Phe Lys Ser Met Gln Gly Asp Gly Val
            195                 200                 205
Leu Phe His Gly Glu Gly Gln Arg Gly Asp His Ile Thr Leu Glu Leu
    210                 215                 220
Gln Lys Gly Arg Leu Ala Leu His Leu Asn Leu Gly Asp Ser Lys Ala
225                 230                 235                 240
Arg Leu Ser Ser Ser Leu Pro Ser Ala Thr Leu Gly Ser Leu Leu Asp
```

```
                    245                      250                      255
    Asp Gln His Trp His Ser Val Leu Ile Glu Arg Val Gly Lys Gln Val
                260                      265                      270
    Asn Phe Thr Val Asp Lys His Thr Gln His Phe Arg Thr Lys Gly Glu
                275                      280                      285
    Thr Asp Ala Leu Asp Ile Asp Tyr Glu Leu Ser Phe Gly Gly Ile Pro
            290                      295                      300
    Val Pro Gly Lys Pro Gly Thr Phe Leu Lys Lys Asn Phe His Gly Cys
    305                      310                      315                      320
    Ile Glu Asn Leu Tyr Tyr Asn Gly Val Asn Ile Ile Asp Leu Ala Lys
                        325                      330                      335
    Arg Arg Lys His Gln Ile Tyr Thr Val Gly Asn Val Thr Phe Ser Cys
                340                      345                      350
    Ser Glu Pro Gln Ile Val Pro Ile Thr Phe Val Asn Ser Ser Gly Ser
                355                      360                      365
    Tyr Leu Leu Leu Pro Gly Thr Pro Gln Ile Asp Gly Leu Ser Val Ser
            370                      375                      380
    Phe Gln Phe Arg Thr Trp Asn Lys Asp Gly Leu Leu Leu Ser Thr Glu
    385                      390                      395                      400
    Leu Ser Glu Gly Ser Gly Thr Leu Leu Leu Ser Leu Glu Gly Gly Ile
                        405                      410                      415
    Leu Arg Leu Val Ile Gln Lys Met Thr Glu Arg Val Ala Glu Ile Leu
                420                      425                      430
    Thr Gly Ser Asn Leu Asn Asp Gly Leu Trp His Ser Val Ser Ile Asn
            435                      440                      445
    Ala Arg Arg Asn Arg Ile Thr Leu Thr Leu Asp Asp Glu Ala Ala Pro
            450                      455                      460
    Pro Ala Pro Asp Ser Thr Trp Val Gln Ile Tyr Ser Gly Asn Ser Tyr
    465                      470                      475                      480
    Tyr Phe Gly Gly Cys Pro Asp Asn Leu Thr Asp Ser Gln Cys Leu Asn
                        485                      490                      495
    Pro Ile Lys Ala Phe Gln Gly Cys Met Arg Leu Ile Phe Ile Asp Asn
                500                      505                      510
    Gln Pro Lys Asp Leu Ile Ser Val Gln Gln Gly Ser Leu Gly Asn Phe
            515                      520                      525
    Ser Asp Leu His Ile Asp Leu Cys Ser Ile Lys Asp Arg Cys Leu Pro
            530                      535                      540
    Asn Tyr Cys Glu His Gly Gly Ser Cys Ser Gln Ser Trp Thr Thr Phe
    545                      550                      555                      560
    Tyr Cys Asn Cys Ser Asp Thr Ser Tyr Thr Gly Ala Thr Cys His Asn
                        565                      570                      575
    Ser Ile Tyr Glu Gln Ser Cys Glu Val Tyr Arg His Gln Gly Asn Thr
                580                      585                      590
    Ala Gly Phe Phe Tyr Ile Asp Ser Asp Gly Ser Gly Pro Leu Gly Pro
                595                      600                      605
    Leu Gln Val Tyr Cys Asn Ile Thr Glu Asp Lys Ile Trp Thr Ser Val
            610                      615                      620
    Gln His Asn Asn Thr Glu Leu Thr Arg Val Arg Gly Ala Asn Pro Glu
    625                      630                      635                      640
    Lys Pro Tyr Ala Met Ala Leu Asp Tyr Gly Gly Ser Met Glu Gln Leu
                        645                      650                      655
    Glu Ala Val Ile Asp Gly Ser Glu His Cys Glu Gln Glu Val Ala Tyr
                660                      665                      670
    His Cys Arg Arg Ser Arg Leu Leu Asn Thr Pro Asp Gly Thr Pro Phe
            675                      680                      685
    Thr Trp Trp Ile Gly Arg Ser Asn Glu Arg His Pro Tyr Trp Gly Gly
```

30/37

```
            690                     695                     700
Ser Pro Pro Gly Val Gln Gln Cys Glu Cys Gly Leu Asp Glu Ser Cys
705                     710                     715                     720
Leu Asp Ile Gln His Phe Cys Asn Cys Asp Ala Asp Lys Asp Glu Trp
                    725                     730                     735
Thr Asn Asp Thr Gly Phe Leu Ser Phe Lys Asp His Leu Pro Val Thr
                    740                     745                     750
Gln Ile Val Ile Thr Asp Thr Asp Arg Ser Asn Ser Glu Ala Ala Trp
                755                     760                     765
Arg Ile Gly Pro Leu Arg Cys Tyr Gly Asp Arg Arg Phe Trp Asn Ala
                770                     775                     780
Val Ser Phe Tyr Thr Glu Ala Ser Tyr Leu His Phe Pro Thr Phe His
785                     790                     795                     800
Ala Glu Phe Ser Ala Asp Ile Ser Phe Phe Phe Lys Thr Thr Ala Leu
                    805                     810                     815
Ser Gly Val Phe Leu Glu Asn Leu Gly Ile Lys Asp Phe Ile Arg Leu
                    820                     825                     830
Glu Ile Ser Ser Pro Ser Glu Ile Thr Phe Ala Ile Asp Val Gly Asn
                    835                     840                     845
Gly Pro Val Glu Leu Val Val Gln Ser Pro Ser Leu Leu Asn Asp Asn
        850                     855                     860
Gln Trp His Tyr Val Arg Ala Glu Arg Asn Leu Lys Glu Thr Ser Leu
865                     870                     875                     880
Gln Val Asp Asn Leu Pro Arg Ser Thr Arg Glu Thr Ser Glu Glu Gly
                    885                     890                     895
His Phe Arg Leu Gln Leu Asn Ser Gln Leu Phe Val Gly Gly Thr Ser
                    900                     905                     910
Ser Arg Gln Lys Gly Phe Leu Gly Cys Ile Arg Ser Leu His Leu Asn
            915                     920                     925
Gly Gln Lys Met Asp Leu Glu Glu Arg Ala Lys Val Thr Ser Gly Val
        930                     935                     940
Arg Pro Gly Cys Pro Gly His Cys Ser Ser Tyr Gly Ser Ile Cys His
945                     950                     955                     960
Asn Gly Gly Lys Cys Val Glu Lys His Asn Gly Tyr Leu Cys Asp Cys
                    965                     970                     975
Thr Asn Ser Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val Ser Ala
                    980                     985                     990
Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu Pro Tyr
                995                     1000                    1005
Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr Thr Asp
        1010                    1015                    1020
Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr Thr Gln
1025                    1030                    1035                    1040
Ala Pro Ser Leu Leu Leu Phe Ile Asn Ser Ser Ser Gln Asp Phe Val
                    1045                    1050                    1055
Val Val Leu Leu Cys Lys Asn Gly Ser Leu Gln Val Arg Tyr His Leu
                1060                    1065                    1070
Asn Lys Glu Glu Thr His Val Phe Thr Ile Asp Ala Asp Asn Phe Ala
            1075                    1080                    1085
Asn Arg Arg Met His His Leu Lys Ile Asn Arg Glu Gly Arg Glu Leu
        1090                    1095                    1100
Thr Ile Gln Met Asp Gln Gln Leu Arg Leu Ser Tyr Asn Phe Ser Pro
1105                    1110                    1115                    1120
Glu Val Glu Phe Arg Val Ile Arg Ser Leu Thr Leu Gly Lys Val Thr
                    1125                    1130                    1135
Glu Asn Leu Gly Leu Asp Ser Glu Val Ala Lys Ala Asn Ala Met Gly
```

```
              1140                    1145                      1150
Phe Ala Gly Cys Met Ser Ser Val Gln Tyr Asn His Ile Ala Pro Leu
          1155                    1160                    1165
Lys Ala Ala Leu Arg His Ala Thr Val Ala Pro Val Thr Val His Gly
      1170                    1175                    1180
Thr Leu Thr Glu Ser Ser Cys Gly Phe Met Val Asp Ser Asp Val Asn
1185                    1190                    1195                    1200
Ala Val Thr Thr Val His Ser Ser Ser Asp Pro Phe Gly Lys Thr Asp
                  1205                    1210                    1215
Glu Arg Glu Pro Leu Thr Asn Ala Val Arg Ser Asp Ser Ala Val Ile
              1220                    1225                    1230
Gly Gly Val Ile Ala Val Val Ile Phe Ile Ile Phe Cys Ile Ile Gly
          1235                    1240                    1245
Ile Met Thr Arg Phe Leu Tyr Gln His Lys Gln Ser His Arg Thr Ser
      1250                    1255                    1260
Gln Met Lys Glu Lys Glu Tyr Pro Glu Asn Leu Asp Ser Ser Phe Arg
1265                    1270                    1275                    1280
Asn Glu Ile Asp Leu Gln Asn Thr Val Ser Glu Cys Lys Arg Glu Tyr
              1285                    1290                    1295
Phe Ile
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<210> 25
<211> 3528
<212> DNA
<213> Homo sapiens

<400> 25

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cgctttgtgc ccctggaatg gaatcccagt gggaagattg gcatgagagt cgaggtctac        120
ggatgttcct ataaatcaga cgttgctgac tttgatggcc gaagctcact tctgtacagg        180
ttcaatcaga agttgatgag tactctcaaa gatgtgatct ccctgaagtt caagagcatg        240
caaggagatg gggtcctgtt ccatggagaa ggtcagcgtg gagaccacat caccttggaa        300
ctccagaagg ggaggctcgc cctacacctc aatttgggtg acagcaaagc gcggctcagc        360
agcagcttgc cctctgccac cctgggcagc ctcctggatg accagcactg gcactcggtc        420
ctcattgagc gggtgggcaa gcaggtgaac ttcacggtgg acaagcacac acagcacttc        480
cgcaccaagg gcgagacgga tgccttagac attgactatg agcttagttt tggaggaatt        540
ccagtaccag gaaaacctgg gaccttttta aagaaaaact ccatggatg catcgaaaac         600
ctttactaca atggagtaaa cataattgac ctggctaaga gacgaaagca tcagatctat        660
actgtgggca atgtcacttt ttcctgctcc gaaccacaga ttgtgcccat cacatttgtc        720
aactccagcg gcagctattt gctgctgccc ggcaccccc aaattgatgg ctctcagtg          780
agtttccagt ttcgaacatg gaacaaggat ggtctgcttc tgtccacaga gctgtctgag        840
ggctcgggaa ccctgctgct gagcctggag ggtggaatcc tgagactcgt gattcagaaa        900
atgacagaac gcgtagctga aatcctcaca ggcagcaact gaatgatgg cctgtggcac         960
tcggttagca tcaacgccag gaggaaccgc atcacgctca ctctggatga tgaagcagca       1020
cccccggctc cagacagcac ttgggtgcag atttattctg gaaatagcta ctattttgga       1080
gggtgccccg acaatctcac cgattcccaa tgtttaaatc ccattaaggc tttccaaggc       1140
tgcatgaggc tcatctttat tgataaccag cccaaggacc tcatttcagt tcagcaaggt       1200
tccctgggga attttagtga tttacacatt gatctgtgta gcatcaaaga caggtgtttg       1260
ccaaactact gtgaacatgg aggaagctgc tcccagtcct ggactacctt ctattgtaac       1320
tgcagtgaca caagttacac tggtgccacc tgccacaact ccatctacga gcaatcctgc       1380
gaggtgtaca ggcaccaggg gaatacagcc ggcttcttct acatcgactc agatggcagc       1440
ggcccactgg gacctctcca ggtgtactgc aatatcactg aggacaagat ctggacatca       1500
gtgcagcaca acaatacaga gctgacccga gtgcggggcg ctaacccctga gaagccctat      1560
gccatggcct tggactacgg gggcagcatg aacagctgg aggccgtgat cgacggctct        1620
gagcactgtg agcaggaggt ggcctaccac tgcaggaggt cccgcctgct caacacgccg       1680
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gatggaacac catttacctg gtggattggg cggtccaatg aaaggcaccc ttactgggga    1740
ggttcccctc ctggggtcca gcagtgtgag tgtggcctag acgagagctg cctggacatt    1800
cagcactttt gcaattgcga cgctgacaag gatgaatgga caaatgatac tggctttctt    1860
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tcagaagccg cttggagaat tggtcccttg cgttgctatg gtgaccgacg cttctggaac    1980
gccgtctcat tttatacaga agcctcttac ctccactttc ctaccttcca tgcggaattc    2040
agtgccgata tttccttctt ttttaaaacc acagcattat ccggagtttt cctagaaaat    2100
cttggcatta aagacttcat tcgactcgaa ataagctctc cttcagagat caccttttgcc   2160
atcgatgttg ggaatggtcc tgtggagctt gtagtccagt ctccttctct tctgaatgac    2220
aaccaatggc actatgtccg ggctgagagg aacctcaagg agacctccct gcaggtggac    2280
aaccttccaa ggagcaccag ggagacgtcg gaggagggcc attttcgact gcagctgaac    2340
agccagttgt ttgtaggggg aacgtcatcc agacagaaag gcttcctagg atgcattcgc    2400
tccttacact tgaatggaca gaaaatggac ctggaagaga gggcaaaggt cacatctgga    2460
gtcaggccag gctgccccgg ccactgcagc agctacggca gcatctgcca caacgggggc    2520
aagtgtgtgg agaagcacaa tggctacctg tgtgattgca ccaattcacc ttatgaaggg    2580
ccctttgca aaaagaggt ttctgctgtt tttgaggctg gcacgtcggt tacttacatg       2640
tttcaagaac cctatcctgt gaccaagaat ataagcctct catcctcagc tatttacaca    2700
gattcagctc catccaagga aacattgca cttagctttg tgacaaccca ggcacccagt       2760
cttttgctct ttatcaattc ttcttctcag gacttcgtgg ttgttctgct ctgcaagaat    2820
ggaagcttac aggttcgcta tcacctaaac aaggaagaaa cccatgtatt caccattgat    2880
gcagataact ttgctaacag aaggatgcac cacttgaaga ttaaccgaga gggaagagag    2940
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ttcaggggtta taaggtcact caccttgggc aaagtcacag agaatcttgg tttggattct    3060
gaagttgcta aagcaaatgc catgggtttt gctggatgca tgtcttccgt ccagtacaac    3120
cacatagcac cactgaaggc tgccctgcgc catgccactg tcgcgcctgt gactgtccat    3180
gggaccttga cggaatccag ctgtggcttc atggtggact cagatgtgaa tgcagtgacc    3240
acggtgcatt cttcatcaga tccttttggg aagacagatg agcgggaacc actcacaaat    3300
gctgttcgaa gtgattcggc agtcatcgga ggggtgatag cagtggtgat attcatcatc    3360
ttctgtatca tcggcatcat gacccggttc ctctaccagc acaagcagtc acatcgtacg    3420
agccagatga aggagaagga atatccagaa aatttggaca gttccttcag aaatgaaatt    3480
gacttgcaaa acacagtgag cgagtgtaaa cgggaatatt tcatctga                 3528
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<210> 26
<211> 1175
<212> PRT
<213> Homo sapiens

<400> 26
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Met Asn Ala Asp Ser Val Val His His Lys Leu Leu His Ser Val Arg
1               5                   10                  15
Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn Pro Ser Gly Lys
            20                  25                  30
Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr Lys Ser Asp Val
        35                  40                  45
Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg Phe Asn Gln Lys
    50                  55                  60
Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys Phe Lys Ser Met
65                  70                  75                  80
Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln Arg Gly Asp His
                85                  90                  95
Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu His Leu Asn Leu
            100                 105                 110
Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro Ser Ala Thr Leu
        115                 120                 125
Gly Ser Leu Leu Asp Asp Gln His Trp His Ser Val Leu Ile Glu Arg
    130                 135                 140
```

                              33/37
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```
Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His Thr Gln His Phe
145                 150                 155                 160
Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp Tyr Glu Leu Ser
                165                 170                 175
Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr Phe Leu Lys Lys
            180                 185                 190
Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn Gly Val Asn Ile
            195                 200                 205
Ile Asp Leu Ala Lys Arg Arg Lys His Gln Ile Tyr Thr Val Gly Asn
        210                 215                 220
Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro Ile Thr Phe Val
225                 230                 235                 240
Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr Pro Gln Ile Asp
                245                 250                 255
Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn Lys Asp Gly Leu
            260                 265                 270
Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr Leu Leu Leu Ser
            275                 280                 285
Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys Met Thr Glu Arg
        290                 295                 300
Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp Gly Leu Trp His
305                 310                 315                 320
Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr Leu Thr Leu Asp
                325                 330                 335
Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp Val Gln Ile Tyr
            340                 345                 350
Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp Asn Leu Thr Asp
            355                 360                 365
Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly Cys Met Arg Leu
        370                 375                 380
Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser Val Gln Gln Gly
385                 390                 395                 400
Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu Cys Ser Ile Lys
            405                 410                 415
Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly Ser Cys Ser Gln
            420                 425                 430
Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr Ser Tyr Thr Gly
        435                 440                 445
Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys Glu Val Tyr Arg
    450                 455                 460
His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp Ser Asp Gly Ser
465                 470                 475                 480
Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile Thr Glu Asp Lys
            485                 490                 495
Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu Thr Arg Val Arg
            500                 505                 510
Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu Asp Tyr Gly Gly
    515                 520                 525
Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser Glu His Cys Glu
    530                 535                 540
Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu Leu Asn Thr Pro
545                 550                 555                 560
Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser Asn Glu Arg His
            565                 570                 575
Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln Cys Glu Cys Gly
        580                 585                 590
```

34/37

```
Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys Asn Cys Asp Ala
        595                 600                 605
Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu Ser Phe Lys Asp
    610                 615                 620
His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr Asp Arg Ser Asn
625                 630                 635                 640
Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys Tyr Gly Asp Arg
            645                 650                 655
Arg Phe Trp Asn Ala Val Ser Phe Tyr Thr Glu Ala Ser Tyr Leu His
            660                 665                 670
Phe Pro Thr Phe His Ala Glu Phe Ser Ala Asp Ile Ser Phe Phe Phe
        675                 680                 685
Lys Thr Thr Ala Leu Ser Gly Val Phe Leu Glu Asn Leu Gly Ile Lys
    690                 695                 700
Asp Phe Ile Arg Leu Glu Ile Ser Ser Pro Ser Glu Ile Thr Phe Ala
705                 710                 715                 720
Ile Asp Val Gly Asn Gly Pro Val Glu Leu Val Val Gln Ser Pro Ser
            725                 730                 735
Leu Leu Asn Asp Asn Gln Trp His Tyr Val Arg Ala Glu Arg Asn Leu
            740                 745                 750
Lys Glu Thr Ser Leu Gln Val Asp Asn Leu Pro Arg Ser Thr Arg Glu
        755                 760                 765
Thr Ser Glu Glu Gly His Phe Arg Leu Gln Leu Asn Ser Gln Leu Phe
    770                 775                 780
Val Gly Gly Thr Ser Ser Arg Gln Lys Gly Phe Leu Gly Cys Ile Arg
785                 790                 795                 800
Ser Leu His Leu Asn Gly Gln Lys Met Asp Leu Glu Glu Arg Ala Lys
            805                 810                 815
Val Thr Ser Gly Val Arg Pro Gly Cys Pro Gly His Cys Ser Ser Tyr
        820                 825                 830
Gly Ser Ile Cys His Asn Gly Gly Lys Cys Val Glu Lys His Asn Gly
        835                 840                 845
Tyr Leu Cys Asp Cys Thr Asn Ser Pro Tyr Glu Gly Pro Phe Cys Lys
    850                 855                 860
Lys Glu Val Ser Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met
865                 870                 875                 880
Phe Gln Glu Pro Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser
            885                 890                 895
Ala Ile Tyr Thr Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser
            900                 905                 910
Phe Val Thr Thr Gln Ala Pro Ser Leu Leu Leu Phe Ile Asn Ser Ser
        915                 920                 925
Ser Gln Asp Phe Val Val Val Leu Leu Cys Lys Asn Gly Ser Leu Gln
    930                 935                 940
Val Arg Tyr His Leu Asn Lys Glu Glu Thr His Val Phe Thr Ile Asp
945                 950                 955                 960
Ala Asp Asn Phe Ala Asn Arg Arg Met His Leu Lys Ile Asn Arg
            965                 970                 975
Glu Gly Arg Glu Leu Thr Ile Gln Met Asp Gln Gln Leu Arg Leu Ser
            980                 985                 990
Tyr Asn Phe Ser Pro Glu Val Glu Phe Arg Val Ile Arg Ser Leu Thr
        995                 1000                1005
Leu Gly Lys Val Thr Glu Asn Leu Gly Leu Asp Ser Glu Val Ala Lys
    1010                1015                1020
Ala Asn Ala Met Gly Phe Ala Gly Cys Met Ser Ser Val Gln Tyr Asn
1025                1030                1035                1040
```

His Ile Ala Pro Leu Lys Ala Ala Leu Arg His Ala Thr Val Ala Pro
                1045   1050   1055
Val Thr Val His Gly Thr Leu Thr Glu Ser Ser Cys Gly Phe Met Val
                1060   1065   1070
Asp Ser Asp Val Asn Ala Val Thr Thr Val His Ser Ser Ser Asp Pro
            1075   1080   1085
Phe Gly Lys Thr Asp Glu Arg Glu Pro Leu Thr Asn Ala Val Arg Ser
        1090   1095   1100
Asp Ser Ala Val Ile Gly Gly Val Ile Ala Val Val Ile Phe Ile Ile
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